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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 15, 2004, 10:30:21; Search time 8.94737 Seconds (without alignments) 58.196 Million cell updates/sec Run on:

US-09-673-795-2 51 1 SLFEGIDIYT 10 Title: Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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503 AA.

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STANDARD;

RESULT 2 HS70 PENCI ID HS70 PENCI

1 SLFEGIDIYT 10

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43

P55063 rattus norv	P34931 homo sapien	P16627 mus musculu	P53623 pichia angu	Q10265 schizosacch	P53421 pichia angu	P19378 cricetulus	P11142 homo sapien	P08109 mus musculu	P87047 paracoccidi	P09435 saccharomyc	Q90473 brachydanio
HS1A_RAT	HS7H_HUMAN	HS7T MOUSE	HS72_PICAN	HS71_SCHPO	HS71_PICAN	HS7C_CRIGR	HS7C_HUMAN	HS7C_MOUSE	HS70 PARBR	HS73_YEAST	HS7C_BRARE
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	eq)	sequence update)	Heat shock 70 kDa protein (HSP70) (Fragment)		Bukaryota; Metazoa; Nematoda; Chromadorea; Onchocercidae: Onchocerca			043	Rothstein N.M., Higashi G., Yates J.,	"Unchocerca Volvulus heat shock protein 70 is amicrofilaremic individuals from a filariasis.	Mol. Biochem. Parasitol. 33:229-236(1989)	珨,	als	che	pyr:	ō u	ä.		ם מ	or send an email to license@isb-sib.ch).	į					PARTIAL	PAKTIAL			×,	တ္တ		5
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01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Heat shock 70 kDa protein (HSP70).
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                     MEDLINE=97351908; PubMed=9208190;
Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H.;
Wolecular cloning and expression of a Penicillium citrinum allergen
with sequence homology and antigenic crossreactivity to a hsp 70
human heat shock protein.",
clin. Exp. Allergy 27:682-690(1997).
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIJINE-863304452; PubMed=3017985;
Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S.;
"Organization, nucleotide sequence, and transcription of the chicken
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                             Eukaryota, Fungi, Ascomycota, Pezizomycotina, Burotiomycetes, Burotiales, Trichocomaceae, mitosporic Trichocomaceae, Penicillium.
NCBI_TaxID=5077;
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                                                                                      (Fragment)
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                                        16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Heat shock 70 kDa protein (Allergen Pen c 19)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; HSP70; 1.
PROSITE; PS00297; HSP70_1; PARTIAL.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Allergen.
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                      Created)
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HSSP; P19120; 3HSC.
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90.0%;
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                      (Rel. 40, C
(Rel. 40, I
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                                                                                                                                 Penicillium citrinum.
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Best Local Similarity
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J. Biol. Chem
                      16-0CT-2001
16-0CT-2001
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MEDLINE-95080396; PubMed=7988690;

Asinis I., Angalidis C., Pagoulatos G., Lazaridis I.;

Sainis I., Angalidis C., Pagoulatos G., Lazaridis I.;

Angalidis C., Pagoulatos G., Lazaridis I.;

Angalidis C., Pagoulatos G., Lazaridis I.;

Inducible member of the hap70 gene family.";

PEBS Lett. 355.282-286(1994).

PEBS Lett. 355.282-286(1994).

COPERATION IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE

PREZISTENTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE POLDING

OR NEMLY TRANSLATED POLYPEPTIDES IN THE CYTCSOL AS WELL AS

CORADARIOS. THE HSP70S IN WITTOCHONDERA AND THE ENDOPLASMIC

RETICULUM PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR

PROCESSES THROUGH THEIR ABILITY TO RECCRIZE NONNATIVE

COMPONATIONS OF OTHER PROPERS. THEY BARICITYDE

SEGMENTS WITH A NET HYDROPELS CHARACTER REXPOSED BY POLYPEPTIDES

COMPONATIONS OF OTHER PROPERS.

SEGMENTS WITH A NET HYDROPEL CHARACTER REXPOSED BY POLYPEPTIDES

STREES. INDUCED DAWAGE.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Cercopithecus.
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PRODOM; PRO00089; HSp70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS0139; HSP70_2; 1.
PROSITE; PS0136; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 634 AA, 69750 MW; 4270F7F08D365AEB CRC64;
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1S-DEC-1998 (Rel. 37, Last sequence update)
1S-DEC-1998 (Rel. 37, Last annotation update)
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                                                                                                                                                                                                                                                                                                                             EMBL; J02579; AAA48825.1; -.
                                                                                                                                                                                                                                                                                                                                                                      PIR; A25646; A25646.
HSSP; PO8109; 1CRT:
InterPro; IPRO1023; HSP70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 92.2
Best Local Similarity 90.0
Matches 9, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          289 SLFEGIDFYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
TISSUE=Kidney;
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MEDLINE=97313267; PubMed=9169871;

MEDLINE=97313267; PubMed=9169871;

Johnston M., Hillier L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Hensen K., A Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., A Heuss-Neitzel D., Hilbert H.-W., Miosga T., Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Porteelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Scharfe M., Scharens B., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestarzu L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;

"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97197984; PubMed=9046100; Purnelle B., Goffeau A.; Purnelle B., Goffeau A.; "The sequence of 32kb on the left arm of yeast chromosome XII reveals six known genes, a new member of the seripauperins family and a new ABC transporter homologous to the human multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Slater M.R., Craig B.A.;
"The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-001-1989 (Rel. 11, Created)
01-007-1994 (Rel. 30, last sequence update)
10-007-2003 (Rel. 42, Last annotation update)
Heat shock protein SAA2.
SSA2 OR YILO24C OR 10931.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycetes;
Saccharomycetales; Saccharomycetacese;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                              92.2%; Score 47; DB 1; Length 638; 90.0%; Pred. No. 0.22; ive 0; Mismatches 1; Indels
                                                                                                                                                                         PRINTS; PRO0301; HEATSHCKYO.
PRODOM; PD000089; HSp70; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
SEQUENCE 638 AA; 69920 MW; D55076A0FFAB6AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 638 AA
or send an email to license@isb-sib.ch)
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                                EMBL; X70684; CAA50019.1; -. PIR; S31766; S31766.
                                                                                                                          InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 90.0.
Best Local Similarity 70.0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    284 ŚLFEGIDFYF 293
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                                                                                                    HSSP; P08107; 1HJO.
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1972 YEAST
AC P10592;
DT 01-0UL-1989
DT 01-0CT-1994
DT 10-OCT-2003
DE Heat shock p
GSA2 ON YLLO
OS SACCHATOWYCE
CC EUKRYCTA; F
CC SACCHATOWYCE
CC SACCHATOWYCE
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CC STRAIN=5288C
RX MEDLINE=9719
RA PUTNELIE B-719
RA PUTNELIE B-719
RA PUTNELIE B-719
RA SEQUENCE FRO
CSTRAIN=5288C
RX MEDLINE=9731
RX JOHNSTON M.,
RA BENES NEITZE
RA HEUSS-NEITZE
RA HUGENER M.,
RA UNGERMEGEIS
RA WELLER SAT:8
RA NATURE 387:8
RR NATURE 387:8
RR NATURE 387:8
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"Protein expression during exponential growth in 0.7 M NaCl medium of Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 137:1-8(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Garrels J.I., Futcher B., Kobayaahi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1944) to Swiss-Prot.
-i- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
BNOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA2 CAN PARTICIPATE IN THE
ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
MEDLINE=95203288; PubMed=7895733;
Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B. Volpe T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
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PTM: Phosphorylated.
SIMILARITY: Belongs to the heat shock protein 70 family.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:000947; SSA2.
GO:0009277; C:cell wall (sensu Fungi); IDA.
GO:0005737; C:cellwall DA.
GO:00003739; C:vacuolar membrane (sensu Fungi); IDA.
GO:000373; F:heat shock protein activity; IMP.
GO:0006457; P:protein folding; IMP.
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PROSITE; PS00299; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; ATP-binding; Multigene family; Acetylation; Phosphorylation.

INIT_MET 1 1 ACETYLATION.

MOD RES 1 1 ACETYLATION.
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638 AA; 69338 MW; 23BDDD120C194912 CRC64;
                                                                                                                                                            Electrophoresis 15:1466-1486(1994).
                                                                                                                                                                                                                       SEQUENCE OF 186-195.
STRAIN-ATCC 38531 / Y41;
MEDLINE-97089742; PubMed=8935650;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACETYLATION, AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BMBL; X12927; CAA31394.1; -.
BMBL; Z73129; CAA97472.1; -.
BMBL; X97560; CAA6167.1; -.
BMBL; S20139; S20139.
HSSP; P19120; 3HSC.
GermOnline; 142019; -.
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COMPLUYEAST-2DPAGE; P10592; -
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Pfam; PF00012; HSP70; 1.
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Best Local Similarity
                                                                                                                               database."
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EMBL; M18540; AAA28078.1; -.
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InterPro; IPR001023; Hsp70.
                                                                                                                                                                      EMBL; X61379; CAA43653.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 SLFEGIDFYT 295
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Best Local Similarity
Matches 9; Conserv
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HS7A_CAEEL
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                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Heat shock 70 kDa protein 1 (HSP70-1).
Cryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Actinopterrygii, Neopterygii, Teleostei, Releostei, Bachthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha;
Beloniformes, Adrianichthyidae, Oryzias.
NTEL_TAXID=8090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDILINE=93077053; PubMed=1339375; Sconzo G., Scardina G., Ferraro M.G.; Sconzo G., Scardina G., Ferraro M.G.; "Characterization of a new member of the sea urchin Paracentrotus lividus hsp70 gene family and its expression."; Gene 121:553-358(1992).
-i. SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                          [1] SEQUENCE FROM N.A.
Naruse K., Sakuragi M.;
Naruse K., Sakuragi M.;
Naruse K., Sakuragi M.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-:- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Paracentrotus lividus (Common sea urchin).
Eukaryota, Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.2%; Score 47; DB 1; Length 639; 90.0%; Pred. No. 0.22;
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Pfam; PF00012; HSp70; 1.

PRINTS; PR00301; HEATSHOKT70.

PROSITE; PS00297; HSp70_1; 1.

PROSITE; PS00329; HSP70_1; 1.

PROSITE; PS01329; HSP70_2; 1.

ATP-binding; Heat shock; Mulligene family.

SEQUENCE 639 AA; 70350 MW; 610BTE0DCOEB0534 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-UNN-1994 (Rel. 29, Created)
01-UNN-1994 (Rel. 29, Last sequence update)
01-UNN-1994 (Rel. 29, Last annotation update)
Heat shock 70 kDa protein IV (HSP70 IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               639 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=7656;
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Q06248;
                                             ORYLA
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                      HS71 ORYLA ID HS71 ORY AC Q918\overline{F}9;
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    RESULT 6
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Rhabditidae, Peloderinae, Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDINE-88297155; PubMed=2841196;
Snutch T.P., Heschl M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ..
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Gene 64:241-255(1988).
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                           R HSSP; D1201, JC1391, JC1391, JC1391, JC1391, JC1391, JC1391, JC1391, HSP70.

R HSSP; P19120, 3HSC.

R INTERPROJ IPROJO23; HSP70, 1.

R PERNY PROJO301; HSP70, 1.

DR PROSITE; PS00329; HSP70, 1, 1.

PROSITE; PS00329; HSP70, 1, 1.

R PROSITE; PS00329; HSP70, 2, 1.

RW ATP-binding; Heat shock; Multigene family.

RW ATP-binding; Heat shock; Multigene family.
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PRINTS; PR00301; HEATSHOCK70.
PROSITE; PR00207; HSP70; 1.
PROSITE; PS00329; HSP70 1; 1.
PROSITE; PS01036; HSP70 2; 1.
PROSITE; PS01036; HSP70 3; 1.
SATP-binding; Heat shock; Multigene family.
SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
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01-MAR-1989 (Rel. 10, Last sequence update)
01-FBB-1994 (Rel. 28, Last annotation update)
Heat shock 70 kDa protein A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=94008983; PubMed=8404847; Hartmann H., Lottspeich F., Noegel A., Schleicher M.; Irommler P.R.; Hartmann H., Lottspeich F., Noegel A.A.; Schleicher M.; "The heat shock cognate protein from Dictyostellum affects actin polymerization through interaction with the actin-binding protein
                                             ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309
    DB 1; Length 640;
0.22;
                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                     Dictyostelium discoideum (Slime mold).
Eukaryota, Mycetozoa, Dictyosteliida, Dictyostelium.
NCBI_TaxID=44689;
                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Score 47; DB 1
Pred. No. 0.22;
0; Mismatches
                                                                                                                                                                                                                    640 AA
                                                                                                                                                                                                                                                                                                                Heat shock cognate protein (Aginactin). HSPB OR HSC70.
                                                                                                                                                                                                                    PRT;
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MEDLINE=94043116; PubMed=8226849;
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PIRL; A4897.1; --
PIR; A4897.2; A4897.2
PIR; S37394; S37394.
HSSP; P19120; 3HSC.
SWISS-2DPAGE; P36415; DICTY.
DictyBase, DB0001837; HSP70.
InterPro; IPRO0122; HSP70. 1
PRINTS; PRO0121; HSP70. 1
PROSITE; PS00303, HSP70. 1
PROSITE; PS00329; HSP70. 1
PROSITE; PS00329; HSP70. 1
PROSITE; PS00329; HSP70. 1
PROSITE; PS00329; HSP70. 1
PROSITE; PS00329; HSP70. 1
PROSITE; PS00329; HSP70. 1
PROSITE; PS00329; HSP70. 3
PROSITE; PS00329; HSP70. 3
PROSITE; PS00329; HSP70. 3
                90.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBO J. 12:3763-3771(1993).
                                     9; Conservative
                                                                                                                                                                                                                    STANDARD;
                                                                                                               287 SLFEGIDFYT 296
                                                                            1 SLFEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP-binding; Chaperone CONFLICT 1 29
                Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                             HS7C DICDI
P36415;
  Query Match
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RESULT 1

D AC D10D

D AC D10D

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-1- FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILLIZE PREXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF UNBULY TRANSLATED POLYBEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE BNDOPLASMIC RETICULOW PLAY AN ADDITIONAL ROLE BY PROVIDING A DRIVING FORCE FOR PROTEIN TRANSLOCATION WITH HSP90. THEY PARTICIPATE IN ALL THESE PROCESSES THROUGH THEIR ABILLITY TO RECOGNIZE NONATIVE CONFORMATIONS OF OTHER PROTEINS. THEY BIAN EXTENDED PEPTIDE SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYBEPTIDES DURING TRANSLATION AND MEMBERANE TRANSLOCATION, OR FOLLOWING
                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 kDa heat-shock protein (Hgp70) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
Bovidae, Bovinae, Bos.
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0
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Grosz M.D., Skow L.C., Stone R.T.;
"An Alul Polymorphism at the bovine 70 kD heat-shock protein-1
(HSP70-1) locus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                           Length 640;
N -> T (IN REF. 2).
R -> A (IN REF. 2).
R -> A (IN REF. 2).
S -> A (IN REF. 2).
V -> A (IN REF. 2).
I -> L (IN REF. 2).
F -> P (IN REF. 2).
ZEGEDCZDB96A9F5D CRC64;
                                                                                                                                                                                                                                                                                                              1; Indels
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                                                                                                                                                                                                                                                     DB 1;
0.22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H871 BOVIN STANDARD; PRT; 641 AA. 027975; 027964; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence update) 15-UL-1999 (Rel. 38, Last annotation update) Heat shock 70 kDa protein 1 (HSP70-1).
                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                        47;
No. (
                                                                                                                                                                                                                                                     Score Pred. 1
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TISSUE-Skeletal muscle;
MEDLINE-95126904; PubMed=7826329;
                                                                                                                                                                                                                                                                                                           .
                                                                                                                                                                                                  70499 MW;
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SEQUENCE OF 212-641 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INDUCTION: By heat shock.
                                                                                                                                                                                                                                                     92.28;
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EMBL; U02891; AAA03450.1; -.
                                                                                                                                                                                                                                                                               :%0.06
                                                                                                                                                                                                                                                                                                           9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRESS-INDUCED DAMAGE
                                                                                                                                                                                                                                                                                                                                                                                                               284 SLFEGIDFYT 293
                                                                                                                                                                                                                                                                                                                                                               1 SLFEGIDIYT 10
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                                                                                                                                                                                                                                                                            Local Similarity
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  CONFLICT
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HS71 BOVIN
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Matches
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1HJO; 21-0CT-98
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PIR;
PIR;
PIR;
PDB;
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MEDLINE-22388257; PubMed-12477932;
Strausbeeg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEGUENCE FROM N.A. (HSPAIA AND HSPAIB).
Shina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
Submitted (SEP-1999) to the EMBL/Genbank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE=86016721; PubMed=3931075;
Hunt C., Morimoto R.L.;
"Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";
Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (HSPAIA AND HSPAIB).

Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A.,

Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J.,

Lasky S., Hood L.,

"Sequence of the human major histocompatibility complex class III
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE=91055806; PubMed=1700760;
Milner C.M., Campbell R.D.;
"Structure and expression of the three MHC-linked HSP70 genes.";
Immunogenetics 32:242-251(1990).
                                                                                                                                                                        0;
                                                                                                                                              92.2%; Score 47; DB 1; Length 641; 90.0%; Pred. No. 0.22;
                                                                                                                                                                                                                                                                                    HSP1 HUMAN STANDARD; PRT; 641 AA.
PO8107; P19790; O9UGDL9, O9UGDL9, O9UGDL9, O1-AUG-1988 (Rel. 08, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
10-077-2003 (Rel. 42, Last annotation update)
Heat shock 70 kDa protein 1 (HSP70.1) (HSP70-1).
(HSPA1A OR HSPA1B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
         HSEP, POSIGT, 1EUO.

Interpro; IPR01023; HSP70.

PRINTS, PR00310; HSP70.

PRINTS, PR00301; HSP70.

PROSITE; PS00297; HSP70.1; 1.

PROSITE; PS00239; HSP70.1; 1.

PROSITE; PS01036; HSP70.2; 1.

PROSITE; PS01036; HSP70.2; 1.

ATP-binding, Chaperone; Heat shock; Multigene family.

SEQUENCE 641 AA; 70250 MW; 6D548263E98780F9 CRC64;
                                                                                                                                                                         0; Mismatches
                                                                                                                                                           Local Similarity 90.0 nes 9, Conservative
                                                                                                                                                                                                                        286 SLFEGIDFYT 295
                                                                                                                                                                                                 10
                                                                                                                                                                                                 1 SLFEGIDIYT
                                                                                                                                                                                                                                                                                                                                                                            (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                           HUMAN
                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                              RESULT 11
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MEDLINE=9934376; PubMed=1021620;

A MEDLINE=9934376; PubMed=1021620;

A Scipiuk J., Walsh M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;

A Structure of a new crystal form of human hsp70 ArPase domain.";

Acta Crystallogr. D 55:1105-1107(1999)

1. Acta Crystallogr. D 55:1105-1107(1999)

2. I-FUNCTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE

3. PREMISTERINE PROTEENS AGAINST AGASREGATION AND MEDIATE THE POLDING

OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN ORGANELLES. THE HSP70S IN MITOCHONDRIA AND THE ENDOPLASMIC

RETICULUM PLAY AN ADDITTONAL ROLE BY PROVIDING A DRIVING PORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION PROFESSES THROUGH THEIR ABILITY TO RECOGNIZE NONNATIVE

CONFORMATIONS OF OTHER PROTEINS. THEY BILD EXTENDED PEPTIDES DURING TRANSLATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING

STRESS-INDUCED DAMAGE.

1. INDUCTION: By heat shock.

1. SIMILARITY: Belongs to the heat shock protein 70 family.
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Glbbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Sanilus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      extracts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
"Human major histocompatibility complex contains genes for the major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drabent B., Genthe A., Benecke B.-J.; "In vitro transcription of a human hsp 70 heat shock gene by exprepared from heat-shocked and non-heat-shocked human cells."; Nucleic Acids Res. 14:8933-8949(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heat shock protein HSP70.";
Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-36 AND 360-424 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-22 AND 618-641 FROM N.A. MEDLINE=87066768; Pubmed=3786141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=2538825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EWBL, M59828, AAA63226.1, EWBL, M59828, AAA63227.1; EWBL, AF134726, AAD21816.1; EWBL, AP00503; BAB63200.1; EWBL, AP00503; BAB63200.1; EWBL, M1717, AAA52697.1, EWBL, BC002453; AAH0322.1; EWBL, BC018740; AAH18740.1; EWBL, M2744; AAA5944.1; EWBL, X04676; CAA28381.1; EWBL, X04676; CAA28382.1; EWBL, X04677; CAA28382.1; EWBL, X04677; CAA28382.1; EWBL,
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A45871; A45871.
I59139; I59139.
I79540; I79540.
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I -> V (IN REF. 2).
E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 3;
MISSING (IN REF. 2).
N -> S (IN REF. 3; AAD21815)
                                     MIM; 10550; ...
MIM; 603012; ...
GO; GO:000573; C:cytoplasm; TAS.
GO; GO:0005634; C:mucleus; TAS.
GO; GO:0005634; C:mucleus; TAS.
GO; GO:0006640; P:mRNA catebolism; TAS.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
SWISS-2DPAGE; P08107; HUMAN
   Genew; HGNC:5232; HSPA1A.
Genew; HGNC:5233; HSPA1B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete nucleotide sequence of a porcine HSP70 gene.";
Immunogenetics 35:286-289(1992).

-!-FUNCTION: In cooperation with other chaperones, Hsp70s stabilize preexistent proteins against aggregation and mediate the folding of newly translated polypeptides in the cytosol as well as within organelles. These chaperones participate in all these processes through their ability to recognize nomative conformations of other proteins. They bind extended peptide segments with a net hydrophobic character exposed by polypeptides during translation and membrane translocation, or following stress-induced damage.
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                    Gaps
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Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
NCBL_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDILNE-92175874; FubMed=1339404;
Peelman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J.,
Bouquet Y.H.;
                                                                                                                                                                                                                                 0;
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                                                                                                                                                             Score 47; DB 1; Length 641;
Pred. No. 0.22;
0; Mismatches 1; Indels
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Pred. No. 0.22;
0; Mismatches 1; Indels
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PIR; 335718; 335718.
HSSP; POR107; 1H407.
InterPro; 1RR01023; HSP70; 1.
PRINTS; PR0301; HEATSHOCK70.
PROSITE; PS00297; HSP70; 1.
PROSITE; PS00329; HSP70; 1.
PROSITE; PS01329; HSP70; 1.
PROSITE; PS01329; HSP70; 1.
PROSITE; PS0136; HSP70; 1.
PROSITE; PS0136; HSP70; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
SEQUENCE 641 AA; 70083 MW; FE77BB20A03E0A33 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 12
HS71 PIG STANDARD; PRT; 641 AA.
AC P34930;
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DF 01-NOV-1997 (Rel. 35, Last annotation update)
DF Heat shock 70 kDa protein 1 (HSP70.1).
                                                                                                                                                       92.2%;
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Best Local Similarity
Matches 9; Conserv
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hsp70 gene.";
Biochim. Biophys. Acta 1219:64-72(1994).
Biochim. Biophys. Acta 1219:64-72(1994).

-! FUNCTION: In cooperation with other chaperones, Hsp70s stabilize preexistent proteins against aggregation and mediate the folding of newly translated polypeptides in the cytosol as well as within organelles. These chaperones participate in all these processes through their ability to recognize nonnative conformations of other proteins. They bind extended peptide segments with a net hydrophobic character exposed by polypeptides during translation and membrane translocation, or following stress-induced damage.
-! INDUCTION: By heat shock.
-! SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                        TISSUE=Brain;
MEDIINE=94096443; PubMed=8271311;
Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J.,
Massa S.M., Sharp F.R.;
"cDNA cloning and expression of stress-inducible rat hsp70 in normal
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=LEW.1W/GUN;
MEDLINE=95012453; PubMed=7927536;
Walter L., Rauh F., Guenther E.;
"Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STASSUE-Liver; STRAIN=Sprague-Dawley; TISSUE-Liver; MEDLINE-94368974; PubMed=8086479; Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.; "Cloning, nucleotide sequence and expression of rat heat inducible "Cloning, nucleotide sequence and expression of rat heat inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMEL; X77208; CAA54423.1; -.
EMEL; X77208; CAA54423.1; -.
EMEL; X74271; CAA52422.1; -.
EMEL; X74271; CAA5422.1; -.
FIR, 154542; 154542.
InterPro; 1580012; HAP70.
R PFODOM; PRO0012; HSP70, 1.
R PROSITE; PS00297; HSP70, 1.
R PROSITE; PS002097; HSP70, 1.
                                                                 Q07439; P42883;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
14-6-CT-2001 (Rel. 40, Last annotation update)
18-70-1 AND HSP70-2.
                                                    641 AA
                                                    PRT;
                                                                                                                                                                                                                                                                                                                                  J. Neurosci. Res. 36:325-335(1993)
[2]
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                                                    STANDARD;
                                                                                                                                                            Rattus norvegicus (Rat).
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                           NCBI_TaxID=10116;
                                     HS71 RAT
ID HS71 RAT
                       RESULT 13
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STRAIN=22802 / AB972;
MEDLINE=95028152; PubMed=7941740;
MEDLINE=95028152; PubMed=7941740;
MEDLINE=95028152; PubMed=7941740;
MEDLINE=95028152; PubMed=7941740;
M., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
Delaney S., Ouellette B.F.F., Barton A.B., Kaback D.B., Bussey H.;
"Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of the 42 kbp SPO7-CENI-CDC15 region.";
Yeast 10:535-541(1994).
                                                                                                                                                               Gaps
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Garrels J.I., Putcher B., Kobayashi R., Latter G.I., Schwender B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Slater M.R., Craig E.A.; "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae."; Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 590-641 FROM N.A.
MEDLINE=85807943; PubMed=6056826;
Ogden R.C., Lee M.-C., Knapp G.;
"Transfer RNA splicing in Saccharomyces cerevisiae: defining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender F
Volpe T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                            ;
                                                                                                     Score 47; DB 1; Length 641; Pred. No. 0.22;
                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases
227 D -> H (IN REF. 2 AND 3).
108 G -> A (IN REF. 3).
70163 MW; D02D96751C868583 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUL-1999 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last amotation update)
Heat shock protein SSAI (Heat shock protein YG100).
SSAI OR YAL005C.
                                                                                                                                                                                                                                                                                                                                                                                                      641 AA
                                                                                                                                                                  0; Mismatches
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FEMS Microbiol. Lett. 137:1-8(1996)
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MEDLINE=97089742; PubMed=8935650;
Norbeck J., Blomberg A.;
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MEDLINE=95203288; PubMed=7895733;
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90.0%;
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Best Local Similarity 90.0
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  227
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     227 2
408 4
641 AA;
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P10591;
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Search completed: September 15, 2004, 10:34:29 Job time : 9.94737 secs
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DR HERY, X12926; CAA31393.1; -.

DR HSK, L22015; AAC04952.1; ALT_SEQ.

BRIS, 24349; HHRYA1.

BR HSSP; P19120; 31802.

BR Germonline; 138348; -.

BR Germonline; 138348; -.

BR GOOGOOGO TO COORDER; PLO591; -.

BR GO, GOOGOOGO TO COORDER; PLO591; -.

BR GO, GOOGO FOR TO COORDER; DA.

BR GO, GOOGO TO COORDER; DA.

BR GO, GOOGO TO COORDER; DA.

BR GO, GOOGO TO COORDER; DA.

BR GO, GOOGO TO COORDER; DA.

BR GO, GOOGO TO COORDER; DA.

BR GO, GOOGO TO COORDER; DA.

BR GO, GOOGO TO COORDER; DEAT SHOCK PROCESIN ACTIVITY; IDA.

BR GO, GOOGO TO COORDER; DEAT SHOCK PROCESIN ACTIVITY; IDA.

BR GO, GOOGO TO COORDER; DEAT SHOCK PROCESIN ACTIVITY; IDA.

BR GO, GOOGO TO COORDER; DEAT SHOCK PROCESIN ACTIVITY; IDA.

BR GO, GOOGO TO COORDER; DEAT SHOCK PROCESIN ACTIVITY; IDA.

BR INTERFEY PROCESIN; HSAPTO; 1.

BR PROSITE; PROCESIP; MULLIGENE family; Acetylation.

BR HOND RES

BR INIT MET

BR MOD RES

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Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to Swiss-Prot.
-!- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES
BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE
ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST
SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE
ATP-DEPRENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-! SIMILARITY: Belongs to the heat shock protein 70 family.
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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NCBL_TaxID=9913;
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C. -!- FUNCTION: IN COORERATION WITH OTHER CHAPERONES, HSP70S STABILIZE
PREAKISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
OF NEMLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN
ORGANELLES: THE HSP70S IN WITHOCHONDER, AND THE ENDOPLASMIC
ORGANELLES: THE HSP70S IN WITHOCHONDER, AND THE ENDOPLASMIC
ORGANELLES: THE HSP70S IN WITHOCHONDER, AND THE ENDOPLASMIC
PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGNAL TRANSDUCTION
PATHWAYS IN COORERATION WITH HSP90; THEY PRATICIPATE IN ALL THESE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES
COMFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES
COMFORMATION AND MEMBRANE TRANSLOCATION, OR FOLLOWING
STRESS-INDUCED DAMAGE.
-!- INDUCTION: By heat shock.
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                        TISSUE-Liver;
MEDLINE=94070117; PubMed=8249428;
Kowalski J., Gilbert S.A., van Drunen-Littel-Van den Hurk S.,
van den Hurk J., Babiuk L.A., Zamb T.J.;
"Heat-shock promoter-driven synthesis of secreted bovine herpesvirus
glycoproteins in transfected cells.";
Vaccine 11:1100-1107[1993].
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Grosz M.D., Skow L.C.;
Submitted (JAN-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   shock; Multigene family.; 229C19EEBBF610DF CRC64;
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90.0%; Pred. No. 0.22;
iive 0; Mismatches :
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Plan, PF00012; HSP70; 1.
PRINTS, PR00301; HBATSHCK70.
ProDom; PD000089; HSP70; 1.
PROSITE; PS003297; HSP70 1; 1.
PROSITE; PS003295; HSP70 2; 1.
PROSITE; PS01036; HSP70 3; 1.
ATP-binding; Chaperone; Heat shoc SEQUENCE 641 AA; 70228 MW; 2;
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SEQUENCE OF 1-28 FROM N.A.
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Q9u667 littorina p
Q9u669 littorina s
Q9u669 littorina s
Q9u669 littorina p
Q9u666 littorina p
Q9u666 littorina p
Q9u666 littorina p
P81159 aplysia cal
Q90520 oncorhynchu
Q9899 fugu rubrip
Q81508 cetorhinus
Q83718 rattus ratt
Q8jhm4 pseudocarch
Q8jhm4 pseudocarch
Q8jhm9 alopias sup
Q8jhs0 alopias sup
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                                                   September 15, 2004, 10:30:46; Search time 36.3158 Seconds (without alignments) 86.882 Million cell updates/sec
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                                                                                                                                                                          1017041
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                      Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
                               OM protein - protein search, using sw model
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Q9U669
Q9U665
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Q90520
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sp_plant:*
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sp_plant:*
sp_rodent:*
sp_vortebrate:*
sp_vortebrate:*
sp_unclassified:*
sp_vortus:*
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Gapop 10.0 , Gapext 0.5
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1: Sp_archea:*
2: Sp_bacteria:*
3: Sp_fungi:*
4: Sp_human:*
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seq length: 200000000
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Perfect score:
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Maximum DB
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	Q8jhq7 lamna ditro Q8jhq0 megachasma Q8jhp4 mitsukurina Q8jhq3 lamna ditro Q8jhq3 lamna ditro Q8jhn1 cetorhinus Q8jhs9 odontaspis	Vejhtq coontaspis Qejhtq lamma ditro Qejhtq lamma ditro Qejhto lamma ditro Qejhto lamma ditro Qejhtq lamma ditro Qejhtq lamma ditro Qejhtq lamma ditro Qejhtq lamma ditro	OBJES alopias per QBJES alopias per QBJES alopias per QBJES alopias per QBJES QBJES alopias sup QBJES alopias sup QBJES alopias sup QBJES alopias sup QBJES alopias sup QBJES alopias per QBJES Alopias per QBJES	08jhp2 mitsukurina 08jhp3 mitsukurina 08jhs5 alopias pel 08jhn5 pseudocarch 08jhp6 megachasma
Q8JHR2 Q8JHR8 Q8JHN3 Q8JHR6 Q8JHR6	285427 285420 285420 285423 28543 28543	280414 280429 280480 280486 280486	Q8JHS2 Q8JHS3 Q8JHN7 Q8JHT1 Q8JHR9 Q8JHR3	Q8JHP2 Q8JHS5 Q8JHN5 Q8JHP6
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ALIGNMENTS

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01-MAR-2002 01-MAR-2002 01-OCT-2003

PRELIMINARY;

Q8UWM9

RESULT 1 Q8UWM9

| 1002 (TrEMBLrel. 26, 1002 (TrEMBLrel. 26, 1003 (TrEMBLrel. 26, 1000 to the maculatus (Southersydia) Meazos, Chordata, errygii, Neopeerygii, Neopeerygii, Neopeerygii, Neopeerygii, Neopeerygii, Neopeerygii, Serrygii, Neopeerygii, Neopeerygii, Neopeerygii, Serrygii, Neopeerygii, Serrygii, Neopeerygii, Serrygii, Neopeerygii, Serrygii, Neopeerygii, Serrygii, Neopeerygii, Serrygii, Neopeerygii, Neopeerygii, Neopeerygii, Serrygii, <pre>Duery Match 94.1%; Score 48; DB 13; Length 639; Sest Local Similarity 80.0%; Pred. No. 0.92; datches 8; Conservative 2; Mismatches 0; Indels 0; Gaps</pre> |
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1 SLFEGIDIYT 10

8

Q8JHM8 Q63718 Q8JHN4 Q8JHS0 Q8JHS3

0

0;

Gaps

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Indels

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Littorina scutulata (Checkered periwinkle).

Bukaryota, Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Genogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Littorina plena (Black periwinkle).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBU databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL., AFIGHS10; ARIZJOR9.1; -.
GO; GO: 0005524; F.AIP binding; IEA.
InterPro; IPR001023; Hsp70.
                                                                                                                                                                                                                                                                                                                                                     Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
"ubmitted (CCT-1999) to the EMBL/GenBank/DDBJ databases.
submitted (CCT-1999) to THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AF191826; AAF12785.1; -.
GO, GO:005224; F:ATP binding; IEA.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 47; DB 5; Length 155; Pred. No. 0.31; 1; Indels
     Score 47; DB 5; Length 153;
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Last annotation update)
                                                                                                                                                                                    01.MAY-2000 (TrEMBLrel. 13, Created)
01.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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                                                                                                                                                           155 AA
                                  0; Mismatches
                     Pred. No.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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PROSITE; PS01036; HSP70_3; 1.
ATP-binding.
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       92.2%;
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Best Local Similarity 90..

Best Local Similarity 90..
       Query Match
Best Local Similarity 90.0°
Matches 9; Conservative
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                                                                               80 SLFEGIDFYT 89
                                                               1 SLFEGIDIYT 10
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SEQUENCE
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Q9U665;
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Q9U669
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Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                             Littorina plena (Black periwinkle).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                          Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
"Heat-shock genes in the bubl/Genbank/DDBJ databases.
submitted (OCT-1999) to the EMBL/Genbank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AFI91825; AAFI2784.1; -.
GO; GO:0005524; FAIP binding; IEA.
InterPro; IPR001023; HSp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92.2%; Score 47; DB 5; Length 146; 90.0%; Pred. No. 0.29; ive 0; Mismatches 1; Indels
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153 153
153 AA, 17352 MW, E29EE20C4CAF934D CRC64,
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16607 MW; C3F3556A1AF438BB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat-shock protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 AA.
                                                                   146 AA
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ProDom; PD000089; HSP70; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding. 1.
NOW TER 1.
SEQUENCE 153 AA; 17352 MW;
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Matches 9; Conservative
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                                                                   PRELIMINARY;
288 SLFEGVDLYT 297
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T. "Hear-shock games in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
RESI, AF191829; AAF12788.1; -.
GO; GO: 0005524; F:ATP binding; IEA.
R InterPro; IPRO1012; HSP70.
R PRINTS; PRO0301; HEATSHOCK70.
R PRINTS; PRO0301; HEATSHOCK70.
R PROBON; PRO0089; HSP70, 1.
R PROBON; PRO1089; HSP70, 1.
R PROSITE; PS01036; HSP70, 3; 1.
R ATP-binding.
T NON TER 158 158
C SEQÜENCE 158 AA; 17891 MW; B41E5356BCECAD2F CRC64;
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                  SEQUENCE FROM N.A. Hohenlohe P.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                      THEALT-Shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
C -1 SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; AR191824; AAF12783.1; -..
GO; GO:0005224; F.AFP binding; IEA.
InterPro; IPR001023; HSp70.
R Pfam; PR00310; HEATSHOCK70.
R ProDom; PR000089; HSp70; 1.
R PROSITE; P801036; HSp70; 1.
R PROSITE; P801036; HSp70; 1.
T NON TER 158 158
C SEQUENCE 158 AA; 17887 NW; B41E5356A24CAD2F CRC64;
                                                                                                                                      6
                                                                                                                                                                                                                                                                                                                           Littorina scutulata (Checkered periwinkle).
Bukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
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Bukaryota, Metazoa; Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
                                                                                                          92.2%; Score 47; DB 5; Length 157; 90.0%; Pred. No. 0.31; ative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.2%; Score 47; DB 5; Length 158; 90.0%; Pred. No. 0.31; ive 0; Mismatches 1; Indels
                                                          01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat-shock protein (Fragment).
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
ProDom; PD000089; HSP70; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                      Heat-shock protein (Fragment).
                                                                                                          Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity
9; Conserve
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                                                ATP-binding.
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SEQUENCE
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Q9U666;
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Q9U671
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Hohenlohe P.A.;

"Heat-shock genes in the heat-stressed genus Littorina.";

"Heat-shock genes in the heat-stressed genus Littorina.";

"Heat-shock genes in the BMBL/GenBank/DDBJ databases.

"LountLarITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.

R GO, GO:005524; F:ATP binding; IEA.

R PFANTY: PROMO102; HSP70.

R PFANTY: PROMO102; HSP70.

R PFODON; PROMO103; HSP70.

R PFODON; PROMO1036; HSP70.

R PFODON; PROMO1036; HSP70.

R PFODON; PROMO1036; HSP70.

T NON TER

I NON TER

S SEQUENCE 158 AA; 17868 MW; D2ECE71042EC44CB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Littorina plena (Black periwinkle).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
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       Length 158;
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                                                      Indels
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
92.2%; Score 47; DB 5;
90.0%; Pred. No. 0.31;
tive 0; Mismatches
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90.0%; Pred. No. 0.31;
tive 0; Mismatches ::
                                                                                                                                                                                                                                                                                 158 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P81159;
01-JUN-1998 (TrEMBLrel. 06, Created)
                                                                                                                                                                                                                                                                                                                                                                                                Heat-shock protein (Fragment).
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PROSITE; PS01036; HSP70_3; 1. ATP-binding; Heat shock.
                                                           278
                                                                                                                                                                                           1 SLFEGIDIYT 10
                                                                            278 AA;
                                     NON TER
NON TER
SEQUENCE
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MEDLINE—9307769; PubMed=1360013;

Kuhl D., Kennedy T., Barzilai A., Kandel E.;

Kuhl D., Kennedy T., Barzilai A., Kandel E.;

Tung-term sensitization training in Aplyaia leads to an increase in the expression of BiP, the major protein chaperon of the BR.";

T. Cell Biol. 119:1069-1076(1992).

Cell Biol. 119:1069-1076(1992).

Cell Biol. 119:1069-1076(1992).

Cell Biol. 119:1069-1076(1992).

MEDRIY ELONOR TOWNETHY STRUCK PROTEIN A WIDE VARIETY OF CELLS.

Cell Biol. 119:1069-1076(1992).

REMAILY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.

RESP: P19120; 1BA1.

GO: GO: GO: 0003773; F: heat shock protein activity; IBA.

RICEPTO: PRO1012; HSP70.

REPROSITE: PRO1012; HSP70.

REPROSITE: PRO1030; HSP70.

REPROSITE: PRO1030; HSP70.

REPROSITE: PRO1030; HSP70.

REPROSITE: PRO1030; HSP70.2; I.

REAL SHOCK; MILIGENE ÉAMILY.

ROW TERR.

RO
                                                     Aplysia californica (California sea hare).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Buthyneura; Opisthobranchia; Anaspidea;
Aplysioidea; Aplysiidae; Aplysia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Rainbow trout 70 kDa heat shock protein (Fragment).
Guochynchus mykiss (Rainbow trout) (Salmo gairdheri).
Eukaryota, Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
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MEDITE=85036330; PubMed=6092938;
KCChary R.K., Jones D., Candido B.P.M.;
"70-kilodalton heat shock polypeptides from rainbow trout:
Characterization of CDNA sequences.";
Mol. Cell. Biol. 4:178-1791(1984).
-i- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 47; DB 5; Length 220; Pred. No. 0.45; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24684 MW; FA8557F2BB85C37A CRC64;
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PIR; I51344; I51344.

HSSP; PORIJ7; H470.

GO; GO:0005524; F:ATP binding; IEA.

GG; GO:000373; F:heat shock protein activity; IEA.

InterPro; IPR001023; Hsp70.

PERM, PF00112; HSP70; 1.

PRINTS; PR00301; HEATSHCKR70.

PRODOUW; PD000089; HSP70; 1.

PROSITE; PS00329; HSP70; 1.
     01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Heat shock cognate 71 kDa protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 SLFEGIDFYT 147
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Best Local Similarity
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Alopiidae;
                                                                                                                                                                                                                                                                                                                                                     Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).
Bukaryota; Metazoa: Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Takifugu.
NCBL_TAXID=31033;
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                                    Length 278;
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                                                                       Indels
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30327 MW; E4C745DE5484C17A CRC64;
                                                                                                                                                                                                                                                                             01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
70kD heat shock protein (Fragment).
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Last sequence update)
Last annotation update)
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GO; GO:0003773; F:heat shock protein activity; IEA.
InterPro; IFR001023; Hsp70.
Pfam; PF00012; HSP70; 2.
PRINTS; PR00301; HEATSHOCK70.
                                92.2%; Score 47; DB 13; 90.0%; Pred. No. 0.58;
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                                                                       0; Mismatches
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PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock.

NON TER 367 AA; 40406 MW;
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01-0CT-2002 (TrEMBLrel. 22,
01-0CT-2003 (TrEMBLrel. 25,
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Best Local Similarity 90.0
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HSP70.
                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                               156 SLFEGIDFYT 165
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us-09-673-795-2.rspt

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PRINTS; PR00301; HEATSHOCK70
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                      01-OCT-2002
                                                                                                                                                                                                                                                                                                              01-0CT-2002
01-0CT-2003
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Q8JHS0
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10117;
                                                                                                                                                                                                                                                                                   | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division | Division 
                                                                                                                                                                                                               Martin A.P., Burg T.; "Perils of paralogy: Using Hsp70 genes for inferring organismal
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"Cloning of cDNA for the rat inducible 70KD heat shock protein
"Cloning of cDNA for the rat inducible 70KD heat shock protein
(HSP70).",
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; Z27118; CAA81642.1; -.
HSSP; P08107; 1H30.
GG; GO:0005524; F:ATP binding; IEA.
InterPro; IPR00102; HSP70.
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Angeletti B., Passarelli F., Orru D., Pascale E., Butler R.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.2%; Score 47; DB 13; Length 444; 90.0%; Pred. No. 0.97; 1ve 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           92.2%; Score 47; DB 11; Length 455; 90.0%; Pred. No. 1; 1; Indels iive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50405 MW; 0F45F12CBA1E2971 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Heat shock rotein 70 (Fragment).
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Probom; PD000089; Hsp70; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding. 1 1
NON_TER 455
SEQUENCE 455 AA, 50405 MW; C
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Best Local Similarity
Laca 9; Conserve
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Best Local Similarity
                                                                                                                SEQUENCE FROM N.A.
                                    NCBI_TaxID=57982;
                                                                                                                                                                       STRAIN=Cema6;
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Bukaryota; Metazoa; Chordatei; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes;
Pseudocarchariidae; Pseudocarcharias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alopias superciliosus.
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Alopiidae;
                                                                                                                                                                                                                                                                                                                                                            STRAIN=Pska5;
Martin A.P., Burg T.;
"Perils of paralogy: Using Hsp70 genes for inferring organismal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
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                                                                                                                                                                                                                                                                                                                                                                                                                                         phylogenies.";
Submitted (APR-2002) to the BMBL/GenBank/DDBJ databases.
--- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
BMBL; APSD0488; AAM53196.1;
GO, GO:0005524; F:ATP binding; IEA.
InterPro; IPR001023; HSp70.
Pfam; PP00012; HSP70; 1.
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-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AFSO2452; AAM53160.1; -.
GO; GO:0005524; F:ATP binding; IEA.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        459 459
459 AA; 50209 MW; 0D0055A45248652A CRC64;
                                           (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 25, Last annotation update)
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Last sequence update)
Last annotation update)
459 AA
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PRT;
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ProDom; PD000089; HSP70; 1.
PROSITE; PS00129; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding.

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SEQUENCE 459 AA; 50209 MW; (
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                                                                                                                          Hsp70 protein (Fragment).
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Matches 9; Conservative
PRELIMINARY;
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DR ProDom; PD000089; Hsp70; 1.

DR PROSITE; PS00329; HSP70_2; 1.

DR PROSITE; PS01036; HSP70_2; 1.

KW ATP-binding. 1 1

FT NON TER 461 461

SQ SEQUENCE 461 AA; 50591 MW; 1A9E5B4BC41077FE CRC64;

Query Match

Query Match

Best Local Similarity 90.0%; Pred. No. 1;

Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps

Qy 1 SLFEGIDFYT 255

Db 246 SLFEGIDFYT 255
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Search completed: September 15, 2004, 10:35:44 Job time : 36.3158 secs

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Sequence 125, Appl Sequence 12954, A Sequence 12954, A Sequence 8613, Ap Sequence 8611, Ap Sequence 8611, Ap Sequence 8611, Ap Sequence 326, App Sequence 226, App Sequence 22, App Sequence 22, Appl Sequence 621, Ap Sequence 621, App Sequence 623,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          626, App
52, Appl
53, Appl
54, Appl
55, Appl
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Sequence 12, Appl
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                                                                                                                               2; Search time 45.2632 Seconds (without alignments)
29.609 Million cell updates/sec
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Sequence
Sequence
Sequence
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1: /cgn2 6/ptodata/2/paa/PCT NEW COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US06_NEW COMB.pep:*

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5: /cgn2_6/ptodata/2/paa/US08_NEW COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US08_NEW COMB.pep:*

7: /cgn2_6/ptodata/2/paa/US08_NEW COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-885-523-12
US-60-865-632-12954
US-60-579-062-12954
US-60-579-062-12954
US-60-579-062-12954
US-60-579-062-8613
US-60-581-351-2016
US-60-581-351-2016
US-60-581-351-2016
US-10-501-035-326
US-10-501-035-326
US-10-302-244-1919
US-10-302-242-1219
US-10-302-242-1219
US-10-302-242-1219
US-10-302-242-1219
US-10-302-242-1219
US-60-56-425-623
US-60-56-425-625
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US-60-56-425-625
US-60-570-505-53
US-60-570-505-53
US-60-570-505-53
US-60-570-505-55
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US-60-570-505-55
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                                                                                                                            September 15, 2004, 10:34:32
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Maximum Match 100%
Listing first 45 summaries
                                                                                    - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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51
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Match Length
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Perfect score:
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Result Š. Sequence Sequence Sequence

Sequence 28, Appl Sequence 29, Appl Sequence 30, Appl Sequence 613, Appl Sequence 653, Appl Sequence 655, Appl Sequence 658, Appl Sequence 41, Appl Sequence 42, Appl Sequence 44, Appl Sequence 44, Appl Sequence 10, Appl Sequence 2015, Appl Sequence 2019, Appl Sequence 2016, Appl Sequence 2019, Appl Sequence 2016, Appl Sequence 2016, Appl Sequence 2019, Appl Sequence 2016, Appl Sequen	rr Molecules Associated With ant Improvement	Length 181; ; Indels _0; Gaps 0;	Shock o A Discrete Domain and is
11 7 US-60-576-801-28 12 US-60-576-801-29 11 7 US-60-576-801-30 11 7 US-60-576-812-653 11 7 US-60-576-812-655 11 7 US-60-576-812-655 11 7 US-60-576-812-655 11 7 US-60-592-191-42 11 7 US-60-592-191-42 11 7 US-60-592-191-42 11 7 US-60-592-191-43 11 7 US-60-592-191-44 11 7 US-60-592-191-44 12 US-60-592-191-44 13 US-60-592-191-44 14 7 US-60-581-351-2015 15 US-60-581-351-2015 16 US-60-581-351-2015 17 US-60-581-351-2015 18 US-60-581-351-2015 19 US-60-581-351-2015	WENTS lles and Othe lereof For Pl 701	.2%; Score 47; DB 6; .0%; Pred. No. 0.26; e 0; Mismatches 1	on US/10885523 Joan F.L. n K. Deborah nran N. chard A. n Vivo CTL Elicitation By Heat & Protein Pusion Proteins Maps To CD4+T Cell-Independent 2006-007 2004-007-01 BER: US/09/761,534
27 28 29 30 47 92 31 31 47 92 92 93 94 94 92 92 93 94 94 94 95 96 91 93 94 94 95 96 96 97 97 97 97 97 97 97 97 97 97	RESULT 1 US-10-767-701-33352 ; Sequence 33352, Application US/10767701 ; GENERAL INFORMATION: ; APPLICANT: Kovalic, David K. ; APPLICANT: Cao, Yongwei; TITLE OF INVENTION: Nucleic Acid Molecu; TITLE OF INVENTION: Nucleic Acid Molecu; TITLE OF INVENTION: Dlants and Uses FILE REFERENCE: 38-21(53535)B ; CURRENT APPLICATION NUMBER: US/10/767; ; CURRENT APPLICATION NUMBER: US/10/767; ; SEQ ID NO 33352 LENGTH: 181 ; TYPE: PRT ; CRANISM: SORGHUM bicolor ; FRANURE: ; CATALE INFORMATION: Clone ID: SORBI-289; ; CTATE INFORMATION: Clone ID: SORBI-289; ; CATALE OF TATALES OF TA	Query Match Best Local Similarity Matches 9; Conservat 1 SLFEGIDIYT 1 63 SLFEGIDFYT 7	RESULT 2 S-0-885-523-12 SQUENCE 12, Application US/10885523 GENERAL INFORMATION: APPLICANT: Huang, Qian APPLICANT: Richmond, Joan F.L. APPLICANT: Cho, Bryan K. APPLICANT: Cho, Janzhu K. APPLICANT: Cho, Janzhu K. APPLICANT: Cho, Janzhu K. APPLICANT: Cho, Janzhu K. APPLICANT: Cho, Janzhu K. APPLICANT: Cho, Janzhu K. APPLICANT: Cho, Janzhu K. APPLICANT: Cho, Janzhu K. APPLICANT: Cho, Janzhu K. APPLICANT: Cho, Janzhu K. APPLICANT: Cho, SCO, Janzhu K. APPLICANT: Cho

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APPLICANT: Zhang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions Thereof
TITLE OF INVENTION: Compositions Thereof
TITLE OF INVENTION: Compositions Thereof
TITLE OF INVENTION: Compositions Thereof
TITLE OF INVENTION: 2004-04-03
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
SEQ ID NO 8613
LENGTHUM: ACCORDANCE TO THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRANSMENT OF THE TRAN
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APPLICANT: Baum, James A
APPLICANT: Larosa, Thomas J
APPLICANT: Larosa, Thomas J
APPLICANT: Larosa, Thomas J
APPLICANT: Larosa, Tichifa R. I.
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Rang, Bei
APPLICANT: Zhang, Bei
TITLE OF INVENTION: Compositions thereof
TITLE OF INVENTION: Compositions thereof
TITLE OF INVENTION: 0500515005
TITLE OF INVENTION: 0500515005
TITLE OF INVENTION: 0500515005
TITLE OF INVENTION: 0500515005
TITLE REPRESENCE: 38-01 (5340) 05005
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ. DATE: 2004-06-11
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                                                                                                                                                                                                                                                                         Length 263;
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Pred. No. 0.38;
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CURRENT APPLICATION NUMBER: US/60/579,062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 8613, Application US/60565632 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Baum, James A
Kovalic, David K.
Larosa, Thomas J.
Lu, Maclong
Munyikwa, Tichifa R. I
Roberts, James K.
                                                                                                                                                                                                                                                                                                                                0
                       CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: Patentin version 3.2
SEQ ID NO 12954
LENGTH: 263
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; ORGANISM: Diabrotica virgifera
US-60-565-632-8613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Monsanto Technology,
                                                                                                                                                                                              , ORGANISM: Diabrotica virgifera
US-60-579-062-12954
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Best Local Similarity 90.v-
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Matches 9; Conservative
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TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions Thereof
FILE REFERENCE: 38-21 (53403)B
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
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0.38;
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Pred. No. 0.3;
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US-10-885-523-12
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  PRIOR APPLICATION NUMBER: PCT/US00/32831
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PASKERQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 209
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Pred. No.
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; Sequence 12954, Application US/60579062
; GENERAL INFORMATION:
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APPLICANT: Monsanto Technology, LLC
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Munyikwa, Tichifa R. I.
Roberts, James K.
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APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maclong
APPLICANT: Mnnyikwa, Tichifa R.
APPLICANT: Roberts, James K
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Best Local Similarity 90.0%;
Matches 9; Conservative
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Kovalic, David K.
Larosa, Thomas J.
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Best Local Similarity 90.0
Matches 9; Conservative
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ORGANISM: Unknown
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APPLICANT: CANATY Bei TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and TITLE OF INVENTION: Compositions thereof TITLE REPERBNOE: 38-21 (53403) C CURRENT APPLICATION NUMBER: US/60/579,062 CURRENT FILING DATE: 2004-06-11 NUMBER OF SEQ ID NOS: 41445 SOFTWARE: Patentin version 3.2 SEQ ID NO 8611 DATE: 2004-06-11 ENGINE DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005-06-10 DATE: 2005
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TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REFERENCE: 38-21(53372)
FILE REFERENCE: 38-21(53372)
CURRENT FILING DATE: 2004-06-17
PRIOR APPLICATION NUMBER: US 60/479,962
PRIOR PILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: Patentin version 3.2
SEQ ID NO 2016
LENGTH: 639
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               ; LOCATION: (69)...(69)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid US-60-565-632-8611
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; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-579-062-8611
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Pred. No. 0.95;
0; Mismatches 1; Indels
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Munyikwa, Tichifa R. I.
Roberts, James K
Wu, Wei
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ilarity 90.0%;
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APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maolong
APPLICANT: Munyikwa, Tichifa R
APPLICANT: Roberts, James K
APPLICANT: Roberts, James K
APPLICANT: Zhang, Bei
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                                                                                                               Query Match
Best Local Similarity
Matches 9; Conserv
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APPLICANT: Kovalic, David K.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa, Thomas J.
APPLICANT: Larosa Tichifa R. I.
APPLICANT: Roberts, James K.
APPLICANT: Roberts, James K.
APPLICANT: Roberts, Dames K.
APPLICANT: Roberts, Dames K.
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and TITLE OF INVENTION: Compositions Thereof
TITLE OF INVENTION: 2004-04-27
FILE REFERENCE: 38-21(53403)B
CURRENT APPLICANTION NUMBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
SOFTWARE: Patentin version 3.2
LENGTH: 639
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TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REFERENCE: 38-21(53372)B
CURRENT APPLICATION NUMBER: uS/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR APPLICATION NUMBER: US 60/479,962
PRIOR PLING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2025
LENGTH: 503
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OTHER INFORMATION: Xaa can be any naturally occurring amino acid
FEATURE:
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Pred. No. 0.55;
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                                                         ; TYPE: PRT
; ORGANISM: Diabrotica virgifera
US-60-579-062-8613
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ORGANISM: Diabrotica virgifera
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Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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US-60-565-632-8611
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SEQ ID NO 8613
LENGTH: 376
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APPLICANT: ADAMS, MARK
TITLE OF INVENTION: DEVICES, SUCH AS ARRAYS, COMPRISED OF HUMAN PROTEINS OR PROTEIN
TITLE OF INVENTION: CAPTURE AGENTS, AND USES THEREOF
FILE REPERRNCE: CLOOL381
CURRENT APPLICATION NUMBER: US/10/170,205E
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 40312
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patin Docket Preview
APPLICANT: BOARY, SRAH C.
APPLICANT: BOARY, SRAH C.
APPLICANT: BRISDELL, HUNTS
APPLICANT: ACKMAN, JANET
APPLICANT: ACKMAN, JANET
APPLICANT: WILLIANG, P. MICKEY
APPLICANT: WILLIANG, P. MICKEY
APPLICANT: WOOD WILLIAM I.
APPLICANT: WOOD WILLIAM I.
APPLICANT: WOOD WILLIAM I.
APPLICANT: WOOD WILLIAM I.
APPLICANT: WOOD SET ON THOUSE TO TITLE OF INVENTION: Related Diseases
TITLE OF INVENTION: Related Diseases
TITLE OF INVENTION: Related Diseases
CURRENT APPLICATION NUMBER: US/10/370,715B
CURRENT FILING DATE: 2003-02-21
NUMBER OF SEQ ID NOS: 742
: LENGTH: 641
                                   APPLICANT: Andarmani, Suean
APPLICANT: Andarmani, Suean
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REPRENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT APPLICATION NUMBER: US 60/462,047
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR PILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE pt SEQ genes Version 1.0
SEQ ID NO 1519
LENGTH: 641
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-370-715B-22
Sequence 22, Application US/10370715B
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
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Best Local Similarity 90.0.

Best Local Similarity - 90.0.
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                  TYPE: PRT
CORGANISM: Homo sapiens
US-10-821-234-1519
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US-10-170-205E-32659
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Sequence 326, Application US/10501035
GENERAL INFORMATION:
APPLICANT: Bristol-Myezes Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYBEPTIDE FOR PREDICTING
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT FILING DATE: 2004-07-09
PRIOR PILING DATE: 2002-01-18
NUMBER OF SEQ ID NOS: 795
SOFTWARE: Patentin version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2409, Application US/09949003C
Sequence 2409, Application US/09949003C
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig
APPLICANT: VENTER, J. Craig
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH NEUROPSYCHIATRIC TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: DISORDERS: WOS/949,003C
CURRENT FILING DATE: 2001-09-10
PRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 74065
SOFTMARE: Patentin version 3.2
SEQ ID NO 2409
LENGTH: 641
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Pred. No. 0.95;
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                       Score 47; DB 7; Length 639;
Pred. No. 0.95;
0; Mismatches 1; Indels
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Best Local Similarity 90.0
Matches 9; Conservative
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                          Query Match
Best Local Similarity
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US-09-949-003C-2409
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US-10-501-035-326
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LENGIH: 640
TYPE: PRT
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                                                                                                                                   Query Match 92.2%; Score 47; DB 6; Length 641; Best Local Similarity 90.0%; Pred, No. 0.95; Matches 9; Conservative 0; Mismatches 1; Indels
; SEQ ID NO 32659
; LENGTH: 641
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-205E-32659
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Search completed: September 15, 2004, 10:48:20 Job time : 45.2632 secs

1 SLFEGIDIYT 10 |||||||||| 286 SLFEGIDFYT 295

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

September 15, 2004, 10:31:26 Run on:

% 'search time 12.6316 Seconds (without alignments) 76.152 Million cell updates/sec

US-09-673-795-2 1 SLFEGIDIYT 10 score: Perfect so Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283366 seqs, 96191526 residues Searched:

283366 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	B44261	I51344	T45477	T45479	T45476	T45478	T45471	A25646	A48872	831766	JC1391	\$20139	HHKW7A	A29160	837394	T21394	T43724	853357	\$35718	I54542	A45871	HHBYA1	JH0095	B36590	A45635	151129	T46650	겊	
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%	Query Match																					92.2								
	Score	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47
	Result No.	1	7	e	4	ហ	9	7	α	σι	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

dnaK-tvpe molecula	dnaK-tvpe molecula	dnaK-tvne molecula	dnaK-tvpe molecula	heat-shock protein	heat-shock protein	dnaK-tvne molecula	heat shock protein	dnaK-tvoe molecula	dnaK-tvne molecula	heat shock protein	heat shock protein	dnaK-tvpe molecula	dnaK-tvpe molecula	dnaK-tvne molecula	
A44261	A03309	P00138	I46588	T45473	T45474	JN0668	PC7036	S25585	809036	T45517	JC7132	S48024	S48025	A34041	T45468
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209	214	372	379	467	467	641	641	643	643	651	651	209	209	630	636
90.2	90.2	90.2	90.2	90.2	90.2	90.2	90.2	90.2	90.2	90.2	90.2	86.3	86.3	86.3	86.3
46	46	46	46	46	46	46	46	46	46	46	46	44	44	44	44
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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A, Status: preliminary; not compared with conceptual translation
A, Molecule type: nucleic acid
A, Molecule type: nucleic acid
A, Molecule type: nucleic acid
A, Mote: sequence extracted from NCBI backbone (NCBIP:118950)
C, Genetics:
A, Mote: sequence extracted from NCBI backbone (NCBIP:118950)
C, Genetics:
A, Mote: sequence extracted from NCBI backbone (NCBIP:118950)
C, Genetics:
A, Mote: sequence extracted from NCBI backbone (NCBIP:118950)
C, Sepeription: involved in protein folding and assembling/disassembling of protein compl C, Superfamily: heat shock protein 70
C, Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 208;
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Score 47; DB 2; Pred. No. 0.086; 0; Mismatches 92.2%; 9; Conservative Query Match Best Local Similarity Matches 9; Conserv

1; Indels 1 SLFEGIDIYT 10 ð

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Gaps

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SLFEGIDFYT 141 132

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drak-type molecular chaperone (clone pTH870.7) - rainbow trout (fragment)
Nylternate names: 70K heat shock protein
C;Species: Oncorhynchus mykiss (rainbow trout)
C;Date: 21-Peb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
C;Accession: 151344 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999
R;Kothary, R.K.; Jones, D.; Candido, B.P.M.
Mol. Cell: Biol. 4, 1785-1791, 1984
A;Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization of CA;Reference number: 151344; MUID:85036330; PMID:6092938
A;Accession: 151344
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 151344
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Cross-references: GB:KO2549; NID:g213803; PIDN:AAA49562.1; PID:g213804
C;Function: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone

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RESULT 6
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heat-shock protein 70 [imported] - Funiculina quadrangularis
c;Species: Funiculina quadrangularis
c;Species: Puniculina quadrangularis
c;Accession: T45476
R;Borchiellini, C; Le Parco, Y,
submitted to the EMBL bata Library, September 1997
A;Reference number: Z22983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   heat-shock protein 70 [imported] - Eunicella cavolini (fragment)
C;Species: Eunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T454Pi
R;Borchiellini, C.; Le Parco, Y.
R;Borchiellini, C.; Le EMBL Data Library, September 1997
A;Reference number: Z22983
                                                                                                                                                                                                                                     heat-shock protein 70 [imported] - Chondrosia reniformis (fragment)
C,Species: Chondrosia reniformis
C,Date: 31-Jan_2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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               Length 278;
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                                                          1; Indels
                                                                                                                                                                                                                                                                                                      C; Accession: T45477
R; Borchiellini, C.; Le Parco, Y.
R; Borchiellini, C.; Le Parco, Y.
R; Reference number: Z22983
A; Accession: T45477
A; Status: preliminary; translated from GB/EWBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-467 < BOR>
A; Cross-references: EWBL: AF026517; PIDN: AAC05362.1
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-467 <BOR>
A;Cross: treferences: EMBL;AF026520; PIDN:AAC05364.1
C;Genetics:
               Score 47; DB 2;
Pred. No. 0.12;
0; Mismatches
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C,Superfamily: heat shock protein 70
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C;Superfamily: heat shock protein 70
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Best Local Similarity 90.0%;
Matches 9; Conservative (
                   92.2%;
Query Match
Best Local Similarity 90.0.
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Additional manual chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)
N;Alternate names: heat shock cognate protein 70
C;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Accession: T45471
R;Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.
R;Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.
R;Boves, H.; Mintert, Data Library, September 1997
A;Reference number: Z22980
A;Accession: T45471
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: mRNA
A;Residues: L632 < BOV>
A;Coss-references: BMBL:AF025951; PIDN:AAB81865.1
A;Experimental source: strain AX3
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                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 468;
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A)Accession: T45476
A)Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: mRNA
A)Residues: 1-468 <BOR>
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.2%; Score 47; DB 2; Best Local Similarity 90.0%; Pred. No. 0.21; Matches 9; Conservative 0; Mismatches
                                                                                                                                                                                                      A,Cross-references: EMBL:AF026516; PIDN:AAC05361.1 (Squerics: Hsp70 C;Superfamily: heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: hsc70
A;Note: localized to filopodias and cortex
C;Superfamily: heat shock protein 70
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Matches 9; Conservative
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A; Reference number: S31766

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Score 47; DB 2
Pred. No. 0.3;
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               A;Molecule type: mRNA
A;Residues: 1-638 <SAI>
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Matches 9; Conserv
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Best Local Similarity
Matches 9; Conserv
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A;Accession: S31766
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A;Introns: 61/2
C;Function:
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A)Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein agin

C;Species: Dictyostellum discoideum

C;Species: Dictyostellum discoideum

C;Accession: A48872

R;Eddy, K.J.; Sauterer, R.A.; Condeelis, J.S.

B;Eddy, K.J.; Sauterer, R.A.; Condeelis, J.S.

J. Biol. Chem. 268, 22267-23274, 1993

A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an A;Reference number: A48872; MUID:94043116; PMID:8226849
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N,Alternate names: heat shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 3-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C;Accession: S31766; I36927
R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
submitted to the RMBL Data Library, January 1993
A;Description: Nucleotide sequence of the CDNA encoding a monkey 70kd heat shock protein
                     A25646
Mark-type molecular chaperone - chicken
N/Alternas: heat shock protein 70
C/Species: Gallus gallus (chicken)
C/Species: Gallus gallus (chicken)
C/Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
C/Accession: A25646
R/Morimoto, R.I.; Hunt, C.; Huang, S.Y.; Berg, K.L.; Banerji, S.S.
J. Biol. Chem. 261, 12692-12699, 1986
A/Fitle: Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.
A/Reference number: A25646; MUID:86304452; PMID:3017985
                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Description: involved in protein folding and assembling/disassembling of protein compl
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Molecule type: mRNA
A,Residues: 1-636 <EDD>
A;Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as Va
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C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
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A)Cross-references: GB:J02579; NID:g211940; PIDN:AAA48825.1; PID:g211941
A;Note: the authors translated the codon TCG for residue 583 as Trp
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Pred. No.
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Similarity 90.0%;
9; Conservative
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A;Status: preliminary
                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
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R;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
EASE Lett. 355, 282-286, 1994
A;Title: The hsc70 gene which is slightly induced by heat is the main virus inducible m. A;Reference number: 136927; MUID:95080396; PMID:7988690
A;Accession: 136927
A;Accession: 136927
A;A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Description: involved in protein folding and assembling/disassembling of protein comp; C; Superfamily: heat shock protein 70 C; Keywords: ATP; molecular chaperone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Accession: UC1391 "Cardina, G.; Ferraro, M.G.
Risconzo, G.; Scardina, G.; Ferraro, M.G.
Gene 121, 353-358, 1992
A;Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70
A;Reference number: JC1391; MUID:93077053; PMID:1339375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N'Alternate names: heat shock protein 701V; hsp701V protein
C;Species: Paracentrotus lividus (common urchin)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   dnaK-type molecular chaperone SSA2 - yeast (Saccharomyces cerevisiae)
NyAlternate names: heat shock protein YG102; protein L0971; protein YLL024c
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevision
C;Accession: S20139; S64772; S64775; S69383
R;Slater, Mr.R.; Craig, RA.
Nucleic Acids Res. 17, 805-806, 1989
A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.
A;Reference number: S20139; MUID:89128457; PMID:2644626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                             A;Residues: 1-638 <RES>
A;Cross-references: BMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A;Experimental source: kidney; cell line COS-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dnaK-type molecular chaperone 70IV - sea urchin (Paracentrotus lividus)
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dnaK-type molecular chaperone HSPA1L - human
N.Alternate names: heat shock protein, 70K
C;Species: Homo sapiens (man)
C;Date: 16-Aug-1988 #sequence revision 02-Jul-1996 #text_change 20-Aug-1999
C;Accession: A29160, 137561, 137562
R;Hunt, C: Morimoto, N.I.
Proc. Natl. Acad. Sci. U.S.A. 82, 6455-6459, 1985
A;Pitle: Conserved features of eukaryotic hsp70 genes revealed by comparison with the name on unbers A29160; MUID:86016721, PMID:3931075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A, Roseldues: 1-640 A, Accession: 137561
A, Residues: 1-640 A, Residues: 1-640 A, Residues: 1-640 A, Residues: 1-640 A, Cross-references: GB:MI1717
A, Cross-references: GB:MI1717
B. Gentho: A, Benecke, B. G.
R, Drabent, B.; Gentho, A.; Benecke, B. G.
R, Drabent, B.; Gentho, A.; Benecke, B. G.
Nucleic Acids Res. 14, 893-8948
A, Reference number: 137561
A, Reference number: 137561
A, Reference number: 137561
A, Accession: 137561
A, Rossidues: 1-22 A, Rossidues: 1-22 A, Rossidues: 1-22 A, Rossidues: 1-22 A, Rossidues: 1-22 A, Rossidues: 1-22 A, Rossidues: 1-22 A, Rossidues: 1-22 A, Rossidues: 1-22 A, Rossidues: 1-22 A, Rossidues: 1-22 A, Rossidues: 1-22 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-25 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues: 1-24 A, Rossidues
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C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
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NAlternate names: heat shock cognate protein 70
C;Species: Dictyostelium discoideum
C;Species: JlDec-1993 #sequence_revision 31-Dec-1993 #text_change 20-Aug-1999
C;Accession: 837394
R;Haus, U.; Trommler, P.; Fisher, P.R.; Hartmann, H.; Lottspeich, F.; Noegel, A.A.; Sch EMBO J. 12, 3763-3771, 1993
A;Pitle: The heat shock cognate protein from Dictyostelium affects actin polymerization A;Reference number: 837394; WUID:94008983; PMID:8404847
A;Accession: 837394
A;Molecule type: mRNA
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A;Molecule type: DNA
A;Residues: 616-640 <RE2>
A;Cross-references: EMBL:X04677; NID:g32482; PIDN:CAA28382.1; PID:g32483
C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
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Pred. No. 0.3;
0; Mismatches
                                                                    Score 47; DB 1;
Pred. No. 0.3;
0; Mismatches
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A;Map position: 6p21.3 -6p21.3
A;Introns: #status absent
G;Function:
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                                                                                                                                                   Conservative
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                                                                                                               Best Local Similarity
Matches 9; Conserv
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N;Alternate names: heat shock protein 70 A
S;Speciaes: Caenorhabditis elegans
C;Speciaes: Caenorhabditis elegans
C;Bate: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
C;Accession: JT0285
R;Snutch, T.P.; Heschl, M.F.P.; Baillie, D.L.
Gene 64, 241-255, 1988
A;Fitle: The Caenorhabditis elegans hsp70 gene family: a molecular genetic characterizat
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                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA
A;Residues: 1-639 <GOF>
A;Cross-references: EMBL:Z73129; NID:g1360201; PIDN:CAA97472.1; PID:g1360202; MIPS:YLL02
A;Experimental source: strain S288C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Accession: S64775
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Molecule type: DNA
A, Cross-references: EMEL: Z73129; MIPS: YLL024c
A, Experimental source: strain S288C
A, Experimental source: strain S288C
A; Purnelle, B.; Goffeau, A.
Submitted to the EMEL Data Library, April 1996
A; Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14
mily and a new ABC transporter homologous to the human multidrug resistance protein.
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A;Residues: 1-639 <PUR>
A;Cross-references: EMBL:X97560; NID:g1297003; PIDN:CAA66167.1; PID:g1297007
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A;Reference number: S64775
                                                                                                                          A;Cross-references: EMBL:X12927; NID:g4545; PIDN:CAA31394.1; PID:g4546 R;Goffeau, A.; Purnelle, B. submitted to the Protein. Sequence Database, May 1996 A;Reference number: S64761
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Pred. No. 0.3;
0; Mismatches 1; Indels
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A, Map position: 12L
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Best Local Similarity 90.0%;
Matches 9; Conservative
                                                         A; Status: translation not shown
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                                                                                                 A; Molecule type: DNA
A; Residues: 1-639 <SLA>
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P 15 10:57:57 2004
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A;Residues: 1-640 <HAU>
A;Cross-references: EMBL:X75263; NID:g433874; PIDN:CAA53039.1; PID:g433875
C;Genetics: A;Cross-references: EMBL:X75263; NID:g433874; PIDN:CAA53039.1; PID:g433875
C;Genetics: A;Cross-reference; Nature of Protein folding and assembling/disassembling of protein completises: A;Description: involved in protein 70
C;Superfamily: heat shock protein 70
C;Reywords: ATP; molecular chaperone
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                                                                                                                                                                                                                                                                                                                          0; Gaps
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Search completed: September 15, 2004, 10:36:13 Job time: 12.6316 secs

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September 15, 2004, 10:34:17; Search time 312.632 Seconds (without alignments) 31.221 Million cell updates/sec
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ptodata/2/paa/US107_COMB.pep:*
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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description Π Query Score Match Length DB Result

equence 2, hy equence 2, hy equence 3, hy equence 2552 equence 2247 equence 2253 equence 1208 equence 1208 equence 4961 equence 4961 equence 4961 equence 6435,		aquence 12 equence 64 equence 36 equence 10 equence 26 equence 26 equence 10 equence 26
09-673-795-2 10-110-731-2 10-110-731-3 10-110-731-3 10-244-599-25529 09-791-537-3064 09-791-537-3064 09-791-537-5964 09-791-537-6968 09-791-537-6451 09-791-537-6451 09-791-537-6451 09-791-537-6451 09-791-537-6451	09-791-537-715 00-389-987-763 60-389-987-763 60-389-983-365 10-328-953-326	60-360-033-1236 60-360-033-1236 09-791-537-6434 09-935-625-1043 09-935-625-1847 09-935-625-10847 09-935-625-10847 09-935-625-10847 09-935-625-10847 09-935-625-10847
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ALIGNMENTS

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Sequence 2, Application US/09673795

GENERAL INFORMATION:
APPLICANT: TRIEBEL, FREDERIC
APPLICANT: TRIEBEL, FREDERIC
TITLE OF INVENTION: MUMTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USEFUL IN CANCER
TITLE OF INVENTION: MUMBLE 19069
TITLE OF INVENTION: MAUNOTHERAPY
TITLE OF INVENTION: IMMUNOTHERAPY
TITLE OF INVENTION NUMBER: PS/09/673,795
CURRENT FILING DATE: 1999-04-22
FRIOR FILING DATE: 1999-04-22
FRIOR FILING DATE: 1999-04-22
FRIOR FILING DATE: 1999-04-22
FRIOR APPLICATION NUMBER: FR 98 05033
FRIOR FILING DATE: 1998-04-22
FRIOR FILING DATE: 1998-04-22
FRIOR FILING DATE: 1998-04-22
FRIOR APPLICATION NUMBER: FR 98 05033
FRIOR FILING DATE: 1998-04-22
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FRIOR FILING DATE: 1998-04-22
FRIOR FILING DATE: 1998-04-22
FRIOR FILING DATE: 1998-04-22
FRIOR FILING DATE: 1998-04-2
US-09-673-795-2
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1 SLFEGIDIYT 10
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                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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APPLICANT: TRIBBEL, REDERIC
APPLICANT: GAUDIN, CATHERINE
TITLE OF INVENTION: MUTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USBFUL IN CANCER
TITLE OF INVENTION: IMMUNOTHERAPY
FILE REFERENCE: 03715.0069
CURRENT APPLICATION NUMBER: US/09/673,795
CURRENT APPLICATION NUMBER: PC7/FR99/00957
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: FR 98 05033
PRIOR APPLICATION NUMBER: FR 98 05033
PRIOR FILING DATE: 1998-04-22
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTIN VETS. 2.1
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GENERAL INFORMATION:
APPLICANT: 1.D.M. IMMUNO-DESIGNED MOLECULES
TITLE OF INVENTION: NEW LYMPHOCYTES, A PROCESS FOR PREPARING THE SAME AND
TITLE OF INVENTION: THEIR USE IN THERAPEUTICS
FILE REPERENCE: WOB 99 BA IDM STRE
CURRENT FILING DATE: 1002-04-15
PRIOR APPLICATION NUMBER: US/10/110,731
PRIOR APPLICATION NUMBER: EP 99 120 484.3
PRIOR FILING DATE: 1999-10-15
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                                          0;
Query Match 100.0%; Score 51; DB 20; Length 10; Best Local Similarity 100.0%; Pred. No. 0.0094; Matches 10; Conservative 0; Mismatches 0; Indels
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Pred. No. 0.058;
0; Mismatches
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SRQ ID NO 2
LENGTH: 10
TYPE: PRT
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Best Local Similarity 100.
Matches 10; Conservative
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CORGANISM: Homo sapiens
US-09-673-795-7
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US-10-110-731-2
                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 3
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Best Local Similarity
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US-10-110-731-3
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APPLICANT: La Rosa Thomas J
APPLICANT: Exovalic David K
APPLICANT: Exovalic David K
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(5323)B
CURRENT APPLICATION NUMBER: US/10/424,599
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 255293
LENGTH: 174
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Sequence 22471, Application US/09417507

Sequence 22471, Application US/09417507

Sequence 22471, Application US/09417507

SEQUENCES RELATING TO ASPERGILLUS

TITLE OF INVENTION: FUNICATUS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: PATH99-10

CURRENT APPLICATION NUMBER: US/09/417,507

CURRENT FILING DATE: 1999-10-14

NUMBER OF SEQ ID NOS: 44312

SEQ ID NO 22471
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APPLICANT: I.D.M. IMMUNO-DESIGNED MOLECULES
TITLE OF INVENTION: NEW LYMPHOCYTES, A PROCESS FOR PREPARING THE SAME AND
TITLE OF INVENTION: THEIR UNE IN THERAPEUTICS
FILE REPERRANCE: WOB 99 HEA IDM STRE
CURRENT APPLICATION NUMBER: US/10/110,731
CURRENT FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 10
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US-10-424-599-255293
                                                                                                                                                                                                                                                                                                                                                               DB 27;
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Pred. No. 1.4;
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Pred. No. 0.058;
0; Mismatches
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LOCATION: (1)..(174)
OTHER INFORMATION: unsure at all Xaa locations
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US-10-424-599-255293
; Sequence 255293, Application US/10424599
; GENERAL INFORMATION:
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90.0%;
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Best Local Similarity 90.0.
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Sequence 5964, Application US/09791537
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Desc.
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER TITLE OF INVENTION: WOMBER: US/09/791,537
CURRENT PAPLICATION WOMBER: US/09/791,537
CURRENT PILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
IENGTH: 220
                                                                                                                                                                                                                                                                                                              APPLICANT: Bonazzi, vivien
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
TITLE OF INVENTION: AND USES THEREOF
CURRENT APPLICATION NUMBER: US/60/196,712
CURRENT APPLICATION NUMBER: 0500-0413
NUMBER OF SEQ ID NOS: 3846
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2253
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                                      DB 22; Length 209;
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                                                                                 Indels
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                                  Score 47; DB Pred. No. 1.7; 0; Mismatches
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US-09-791-537-120833
; Sequence 120833, Application US/09791537
; GENERAL INFORMATION:
; APPLICANT: Bionomix, Inc.
; APPLICANT: Debe, Derek
                                                                                                                                                                                                                                                                       Sequence 2253, Application US/60196712 GENERAL INFORMATION:
                               92.2%;
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US-09-791-537-5964
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                           Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
                                                                                                                                                 97 SLFEGIDEYT 106
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Best Local Similarity
Matches 9; Conserv
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; ORGANISM: HUMAN
US-60-196-712-2253
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APPLICANT: Bionomix, inc.
APPLICANT: Bionomix, inc.
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APPLICANT: Bionomix, inc.
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APPLICANT: Bionomix, inc.
APPLICANT: Bionomix, inc.
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 3064
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12, Application US/09761534A

GENERAL INFORMATION:
APPLICANT: Huang, Qian
APPLICANT: Richmond, Joan F.L.
APPLICANT: Richmond, Joan F.L.
APPLICANT: Richmond, Joan F.L.
APPLICANT: Palliser, Deborah
APPLICANT: Cho, Bryan K.
APPLICANT: Cho, Bryan K.
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANT: Cho, Jianzhu
APPLICANTON NUMBER: US/09/761,534A
FILE OF INVENTION: CD4+T Cell-Independent
FILE OF INVENTION: CD4+T Cell-Independent
FILE APPLICATION NUMBER: US/09/761,534A
FILE APPLICATION NUMBER: US/09/761,534A
FRIOR APPLICATION NUMBER: US/09/761,534A
FRIOR APPLICATION NUMBER: US/0116,143
FRIOR FILING DATE: 2000-12-01
FRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 209
TYPE: PPR
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0
                                                                                                        Score 47; DB 18; Length 175;
Pred. No. 1.4;
0; Mismatches 1; Indels
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Pred. No. 1.7;
0; Mismatches 1;
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; OTHER INFORMATION: Murine hsp70 - Segment II
US-09-761-534A-12
                                                                                                                                                                                                                                                                                                                     S-00-791-537-3064
Sequence 3064, Application US/09791537
GENERAL INFORMATION:
                                                                                                        92.2%;
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90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: PRT
; ORGANISM: Aplysia californica
US-09-791-537-3064
                                                                                                 Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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                  ; TYPE: PRT
; ORGANISM: A.fumigatus
US-09-417-507-22471
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 8
US-09-761-534A-12
LENGTH: 175
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Sequence 115866, Application US/09791537

Sequence INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Dancer, Joseph
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT PAPLICATION NUMBER: US/09/791,537
CURRENT PAPLICATION NOWS: 123055
NUMBER OF SEQ ID NOS: 123055
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                       yequence 1, Application US/10328953
gengence 1, Application US/10328953
gengence 1, Application US/10328953
gengence 1, Application General Information of Heat-Shock-Protein-Based Immunotherapies APPLICANT: Hartl, Franz-Ulrich
TILIE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies FILE REFERENCE: 11390/46f01
GURRENT FILING DATE: 2002-12-23
FRIOR APPLICATION NUMBER: US 60/342,570
FRIOR FILING DATE: 2001-12-26
FRIOR FILING DATE: 2001-12-28
FRIOR FILING DATE: 2001-02-88
FRIOR FILING DATE: 2002-04-12
FRIOR FILING DATE: 2002-04-12
FRIOR FILING DATE: 2002-07-29
FRIOR FILING DATE: 2002-07-29
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FRIOR FILING DATE: 2002-07-31
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FRIOR FILING DATE: 2002-07-31
FRIOR FILING DATE: 2002-07-31
FRIOR FRIENG  DATE: 2002-07-31
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank GI:15277246; amino acids 5-381 of hsp70
DATABASE ENTRY DATE: 2001-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                    1; Indels
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90.0%; Pred. No. 3.4;
cive 0; Mismatches 1
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Pred. No. 3.4;
0; Mismatches
Pred. No. 3.3;
                       Mismatches
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90.08;
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Best Local Similarity 90.v
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Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                        268 SLFEGIDFYT 277
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Best Local Similarity
Matches 9; Conserv
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US-09-791-537-115866
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US-09-791-537-115866
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LENGTH: 380
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US-10-328-953-1
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GENERAL INFORMATION:
APPLICANT: Bionomix, Inc.
APPLICANT: Danzer, Joseph
TITLE OF INVENTION: HERE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
TITLE OF INVENTION: METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: PATCHIL Version 3.0
SEQ ID NO 6435
ILENGIA: 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Biomeria, Inc.
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBER
TITLE OF INVENTION: WETHOOS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT PELLING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 49619
       APPLICANT: Danzer, Joseph
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SEQ ID NO 120833
LENGTH: 278
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 22; Length 322;
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                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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Pred. No. 2.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 49619, Application US/09791537 GENERAL INFORMATION:
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US-09-791-537-49619
                                                                                                                                                                                                                                                                                                                                                          92.2%;
90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92.2%;
                                                                                                                                                                                                                                                                                  ) ORGANISM: Oncorhynchus mykiss US-09-791-537-120833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT ORGANISM: Takifugu rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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US-09-791-537-49619
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Search completed: September 15, 2004, 10:46:48 Job time : 312.632 secs

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September 15, 2004, 10:35:52; Search time 90 Seconds (without alignments) 35.632 Million cell updates/sec
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/DEC_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/USO7_NEW_PUB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1335176 segs, 320689617 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 200000000
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51
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Semience 255293	Semience 33350 p	Semience 12. Appl	Segmence 1 Appli	763	Semience 319 App	326	2020	Semience 328, App	329.	330	3466			
SUMMARIES	QI	US-10-424-599-255293	US-10-767-701-33352	US-09-761-534A-12	US-10-328-953-1	US-10-408-765A-763	US-10-328-953-319	US-10-328-953-326	US-10-328-953-327	US-10-328-953-328	US-10-328-953-329	US-10-328-953-330	US-10-108-260A-3466	US-10-369-493-12366	US-10-132-556A-2	US-10-369-493-22298
		12	16	0	12	16	12	42	12	12	12	75	15	15	14	15
	Query Match Length DB	174	181	209	377	380	381	392	393	393	393	405	476	516	622	639
0/0	Query Match	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2	92.2
	Score	47	47	47	47	47	47	47	47	47	47	47	47	47	47	47
	Result No.	Н	7	ო	4	ហ	φ	7	80	σ	10	11	12	13	14	15

Segmence 6233. An	~		- 	Sequence 146. App	ហ	N	ò	0	1	Sequence 1760, Ap		2277		117.	11,	204	396	724.	Sequence 724. App	430	Sequence 43012, A			1753,	47010	3272.	e 3524,	73, Al	7
US-10-369-493-6233	US-10-408-765A-255	09-759-010-3	9-935-6	-039	4	0-316-253-2	3-10-316-25	US-09-761-534A-10	3-10-36	0-369-4	0 - 451 - 4	US-10-369-493-22772	0-369-4	0-447-1	US-09-733-179A-11	US-09-919-039-204	US-10-755-889-396	-7	US-09-925-302-724	-10 - 264	US-10-425-114-43012	US-10-425-114-54413	US-10-408-765A-1256	US-10-408-765A-1753	US-10-767-701-47010	US-10-320-797-3272	US-10-108-260A-3524	US-09-919-039-73	US-10-380-408A-7
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47	47	47	47	47	47	47	47	47	47	47	47	47	47	46	46	46	46	46	46	44	44	44	44	44	44	44	44	44	44
16	17	18	13	20	21	22	23	24	25	26	27	28	53	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 255233, Application US/10424599
Publication No. US20040031072A1
GENERAL INFORMATION:
APPLICANT: LA Royal David K
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
FILE REFERENCE: 38-21(5323)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 255293
LENGTH: 174
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                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: unsure
LOCATION: (1)..(174)
OTHER INFORMATION: unsure at all Xaa locations
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Best Local Similarity
RESULT 1
US-10-424-599-255293
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RESULT 2 US-10-767-701-33352

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GENERAL INVORMENTION:
APPLICANT: Wieland, Felix
APPLICANT: Wieland, Felix
APPLICANT: Wieland, Franz-Ulrich
TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
FILE REFERENCE: 11390/46101
FULE REFERENCE: 11390/46101
CURRENT APPLICATION NUMBER: US 60/342,570
PRIOR APPLICATION NUMBER: US 60/342,570
PRIOR APPLICATION NUMBER: US 60/342,620
PRIOR APPLICATION NUMBER: US 60/343,884
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 60/372,620
PRIOR APPLICATION NUMBER: US 60/399,342
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-28
PRIOR FILING DATE: 2002-07-29-28
NUMBER OF SEQ ID NOS: 331
SOFTWARE: WordPerfect 8:0 for Windows
SEQ ID NO I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank GI:15277246; amino acids 5-381 of hsp70
DATABASE BUTRY DATE: 2001-08-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 763, Application US/10408765A

Sequence 763, Application WS/10408765A

Sublication No. US20040101874A1

GRENEAL INFORMATION:

APPLICANT: Ghosh, Soumitra S.

APPLICANT: Tany, Baing

APPLICANT: Taylor, Steven W.

APPLICANT: Glebn, Gary W.

APPLICANT: Glebn, Gary W.

APPLICANT: Glebn, Gary W.

APPLICANT: Glebn, Gary W.

APPLICANT: Glebn, Gary W.

APPLICANT: Glebn, Gary W.

APPLICANT: Glebn, Gary W.

APPLICANT: Warnock, Dale E.

TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

FILE REFRENCE: 660089.465

CURRENT APPLICATION NUMBER: US/10/408,765A

CURRENT FILING DATE: 2003-04-04

NUMBER OF SEQ ID NOS: 3077

SOFTWARE: FastSEQ for Windows Version 4.0
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US20040071656A1
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Best Local Similarity 90.0.
...... 9, Conservative
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US-10-408-765A-763
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APPLICANT: Chen, Jianzhu

APPLICANT: Eisen, Herman N.

APPLICANT: Eisen, Herman N.

APPLICANT: Eisen, Herman N.

TITLE OF INVENTION: In Vivo CTL Elicitation By Heat Shock

TITLE OF INVENTION: CD4+T Cell-Independent

TITLE OF INVENTION NUMBER: US/09/761,534A

CURRENT APPLICATION NUMBER: DC1/US00/32831

PRIOR APPLICATION NUMBER: US 60/176,143

PRIOR APPLICATION NUMBER: US 60/176,143

PRIOR PILLING DATE: 2000-01-14

NUMBER: OF SEQ ID NOS: 25

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12

LENGTH 209
                                                                                               APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
FILE REFERENCE: 38-21(53535)B
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 33352
LENGTH: 181
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Pred. No. 0.43;
0; Mismatches 1; Indels
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US-10-767-701-33352
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US-09-761-534A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Patent No. US20020146426A1
GENERAL INFORMATION
APPLICANT: Huang, Qian
APPLICANT: Richmond, Joan F.L.
APPLICANT: Cho, Bryan K.
APPLICANT: Cho, Bryan K.
APPLICANT: Cho, Bryan K.
APPLICANT: Cho, Bryan K.
       Sequence 33352, Application US/10767701 Publication No. US20040172684A1 GENERAL INFORMATION:
APPLICANT: Kovalic, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-10-328-953-1
; Sequence 1, Application US/10328953
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Best Local Similarity 90.v
90.v
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Best Local Similarity
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US-09-761-534A-12
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; OTHER INFORMATION: fusion polypeptide: gp100(209-217:Met210)-Gly-Ser-Gly-hsp70(1-38
US-10-328-953-327
                                                                                                                                                                                         Sequence 328, Application US/10328953
Publication No US20040071656A1
GENERAL INFORMATION:
APPLICANT: Wieland, Felix
APPLICANT: Hartl, Franz-Ulrich
TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
FILE REPRENCY: 11390/46L01
CURRENT FILING DATE: 2002-12-23
FRICR APPLICATION NUMBER: US 60/342,570
FRICR PEPTICATION NUMBER: US 60/342,570
FRICR PEPTICATION NUMBER: US 60/342,570
FRICR PEPTICATION NUMBER: US 60/342,570
FRICR FILING DATE: 2001-12-28
FRICR PEPTICATION NUMBER: US 60/342,570
FRICR FILING DATE: 2002-04-12
FRICR PEPTICATION NUMBER: US 60/399,342
FRICR FILING DATE: 2002-04-29
FRICR FILING DATE: 2002-04-29
FRICR FILING DATE: 2002-04-29
FRICR FILING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SOFTWARR: WordPerfect 8.0 for Windows
TYPE: PRI
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    Indels
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    Mismatches
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ORGANISM: Artificial Sequence
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Best Local Similarity 90.0
9; Conservative
                                                                                      285 SLFEGIDFYT 294
                                          1 SLFEGIDIYT 10
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US-10-328-953-327
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Matches
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; OTHER INFORMATION: fusion polypeptide: hsp70(1-381)-Gly-Ser-Gly-gp100(209-217:Met210
US-10-328-953-326
Sequence 319, Application US/10328953

Publication No. US20040071656A1

GENERAL INFORMATION:

APPLICANT: Wieland, Felix

APPLICANT: Hartl, Franz-Ulrich

TITE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies

FILE REFERENCE: 11390/46101

CURRENT APPLICATION NUMBER: US/10/328,953

FRIOR FILING DATE: 2001-12-26

PRIOR PLING DATE: 2001-12-26

PRIOR FILING DATE: 2001-12-26

PRIOR FILING DATE: 2001-12-26

PRIOR FILING DATE: 2001-12-26

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-07-29

PRIOR FILING DATE: 2002-07-30
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Publication No. US20040071656A1
Sequence 336, Application US/10328953
Publication No. US20040071656A1
September 1 US20040071656A1
APPLICANT: Wieland, Felix
APPLICANT: Wateland, Felix
TILLE OF INVENTION: MODULation of Heat-Shock-Protein-Based Immunotherapies
FILE REPERENCE: 11390/46101
CURRENT APPLICATION NUMBER: US/10/328,953
CURRENT APPLICATION NUMBER: US 60/342,570
FRIOR APPLICATION NUMBER: US 60/342,570
FRIOR FILING DATE: 2001-12-26
FRIOR FILING DATE: 2001-04-12
FRIOR FILING DATE: 2002-04-12
FRIOR APPLICATION NUMBER: US 60/372,620
FRIOR APPLICATION NUMBER: US 60/39,342
FRIOR FILING DATE: 2002-04-12
FRIOR FILING DATE: 2002-04-12
FRIOR FILING DATE: 2002-04-13
FRIOR FILING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SECTIVARE: WordPerfect 8.0 for Windows
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; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank GI:15277246; amino acids 1-381 of hsp70
; DATABASE ENTRY DATE: 2001-08-22
US-10-328-953-319
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Pred. No. 0.85;
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Pred. No. 0.87;
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ORGANISM: Artificial Sequence
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Best Local Similarity 90.0-
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Best Local Similarity
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LENGTH: 392
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TYPE: PRT ORGANISM: Aspergillus nidulans
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US-10-108-260A-3466
                                                                                                                                                                                                                                                                                US-10-328-953-330
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LENGTH: 476
                                                                                                                                             LENGTH: 405
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y Squence 329, Application US/10328953
y Publication No. US20040071656A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
TITLE OF INVENTION: WOMBER: US/10/328,953
CURRENT APPLICATION WUMBER: US 60/342,570
PRIOR PRICE APPLICATION NUMBER: US 60/342,570
PRIOR FILING DATE: 2001-12-26
PRIOR PRICE APPLICATION NUMBER: US 60/343,884
PRIOR FILING DATE: 2002-04-12
PRIOR PRILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SOFTWARE: WordPerfect 8.0 for Windows
LEMMIN 393
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US-10-328-953-330

ys-10-328-953-330

ysquence 330, Application US/10328953
ybublication No. US20040071656A1
general information No. US20040071656A1
general information No. US20040071656A1
yapplicant: Wieland, Felix
therefore: Harth, Franz-Ulrich
title REFERENCE: 11390/446101
current Filing DATE: 2002-12-23
yrior Application NUMBER: US 60/342,570
yrior Application NUMBER: US 60/342,570
yrior Application NUMBER: US 60/342,570
yrior Application NUMBER: US 60/342,570
yrior Application NUMBER: US 60/342,570
yrior Application NUMBER: US 60/342,670
yrior Application NUMBER: US 60/342,600
yrior Filing DATE: 2001-12-28
yrior Filing DATE: 2002-04-12
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OTHER INFORMATION: tyrosinase(368-376;Asp370)-Gly-Ser-Gly-hsp70(1-381)
                  FEATURE:
OTHER INFORMATION: fusion polypeptide:
OTHER INFORMATION: hsp70(1-381)-Gly-Ser-Gly-tyrosinase(368-376:Asp370)
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Pred. No. 0.88;
                                                                                                                    Score 47; DB 12; Length 393;
Pred. No. 0.88;
0; Mismatches 1; Indels
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                                                                                                                                92.2%;
ORGANISM: Artificial Sequence
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Best Local Similarity
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US-10-328-953-329
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US-10-328-953-328
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GENERAL INPORMATION:
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THERE OF INVENTION: BARKESTON OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF TITLE OF INVENTION: BLANTS WITH IMPROVED PROPERTIES
FILE REPERRINGE: 38-10 (52052) B
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT FILING DATE: 2003-02-28
FRIOR APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 12366
LENGTH: 516
                                                                                                                                                                                                                                                                                             OTHER INFORMATION: fusion polypeptide: hsp70(1-381)-Gly-Ser-Gly-OTHY-OTHER INFORMATION: gp100(209-217:Met210)-Gly-Ser-Gly-tyrosinase(368-376:Asp370)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3466, Application US/10108260A
Publication No. US20040005560A1
GRNERAL INFORMATION:
APPLICANT: HELLY RESEARCH INSTITUTE
TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
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PRIOR APPLICATION NUMBER: US 60/399,342 PRIOR FILING DATE: 2002-07-29 PRIOR APPLICATION NUMBER: US 60/414,834 PRIOR PILING DATE: 2002-09-28 NUMBER OF SEQ ID NOS: 331 SOFTWARE: WordPerfect 8.0 for Windows SEQ ID NO 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12366, Application US/10369493 Publication No. US20030233675A1
                                                                                                                                                                                                                             TYPE: PRT ORGANISM: Artificial Sequence
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Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
Matches 9; Conservative
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ORGANISM: Homo sapiens
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RESULT 15
US-10-369-493-22298
i Sequence 22284 Application US/10369493
i Sequence 22284 Application No. US20030233675A1
i GENERAL INFORMATION:
i APPLICANT: Cao, Yongwei
i APPLICANT: Hinkle, Gregory J.
APPLICANT: Glodiman, Barry S.
APPLICANT: John NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
SPRIOR FILING DATE: 2002-02-21
NUMBER OF SEQ ID NOS: 47374
LENGTH: 639
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Publication No. US20030082629A1
GENERAL INPORMATION:
APPLICANT: Volloch, Vladimir
APPLICANT: Sherman, Michael
ITILE OF INVENTION: SCREBMING METHODS FOR COMPOUNDS USEFUL
ITILE OF INVENTION: SCREBMING METHODS FOR COMPOUNDS USEFUL
ITILE OF INVENTION: A32367-FCT-USA-A 066290.0106
ICURENT APPLICATION NUMBER: US/10/132,556A
CURRENT FILING DATE: 2002-04-25
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: PCT/US00/07350
PRIOR FILING DATE: 2000-03-17
PRIOR PRILING DATE: 2000-03-17
PRIOR FILING DATE: 4000-03-17
PRIOR PRILING DATE: 4000-03-18
PRIOR PRILING DATE: 1000-03-18
PRIOR PRILING DATE: 2000-03-18
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                                                       92.2%; Score 47; DB 15; Length 516; 90.0%; Pred. No. 1.2; 1:ve 0; Mismatches 1; Indels
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                                                    Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Best Local Similarity 90.0
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Best Local Similarity 90.0
Matches 9; Conservative
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ORGANISM: Homo sapien
US-10-369-493-12366
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US-10-132-556A-2
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LENGTH: 622
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Db 283 SLFEGIDFYT 292
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Search completed: September 15, 2004, 10:51:17 Job time: 90 secs

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Sequence 14, Appl
Sequence 174, Appl
Sequence 5332, Ap
Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
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Sequence 73, Appl
Sequence 72, Appl
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107, App
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Sequence 3, Appli
                                                                          September 15, 2004, 10:32:27; Search time 15.7895 Seconds (without alignments) 32.696 Million cell updates/sec
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(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
(cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
(cgn2_6/ptodata/2/iaa/Perix
(cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
(cgn2_6/ptodata/2/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-441.139-14
US-08-441.139-14
US-09-513-783A-174
US-09-134-000C-5332
US-08-478-89A-19
US-08-478-89A-19
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US-08-637-654-19
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US-08-478-373-107
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US-08-478-373-107
US-08-897-438-107
US-08-897-438-107
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US-08-893-438-107
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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51
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911 4 US-08-649-518-107 913 1 US-08-487-890A-5 913 2 US-08-478-435-5 913 2 US-08-478-435-5 913 2 US-08-478-73-5 913 3 US-08-474-671-5 913 3 US-08-474-671-5 913 4 US-08-6474-671-5 913 4 US-08-837-654-5 913 4 US-08-837-654-5 913 4 US-08-637-763B-6 332 2 US-08-637-763B-6 332 2 US-08-637-763B-6 332 3 US-09-170-354-6 333 2 US-08-938-938-65-52 339 4 US-08-938-692-52 339 4 US-08-938-972-52	THENTS A and David A AND AMINO FABCIUM FOR TCS CORPORAT TO TO TO TO TO TO TO TO TO
8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ALIGN BEULT 1 5-09-107-532A-7125 Sequence 7125, Application US/091075328 Patent No. 6583275 Sequence 7125, Application US/091075328 Sequence 7125, Application US/091075328 Sequence 7125, Application US/091075328 APPLICANT: Lynn A Doucette-Stamm TITLE OF INVENTION: NUCLEIC ACII NUMBER OF SEQUENCES: 7310 CORRESPONDENCES: 7310 CORRESPONDENCES: 7310 CORRESPONDENCES: 7310 CORPUTER: Massachusetts COUNTRY: USA ZITRET: 100 Beaver Street COUNTRY: USA ZITRET: 100 Beaver Street COUNTRY: USA ZITRET: 100 Beaver Street COUNTRY: USA ZITRET: 100 Beaver Street COUNTRY: USA ZITRET: 100 Beaver Street COUNTRY: Waltham STATE: Massachusetts COUNTRY: ABLICAN MEDIUM TYPE: CD/ROM ISO9660 CORPUTER: PC TELEPHON: (781)893-8277 INFORMATION FOR SEQ ID NO: 7125: SEQUENCE CHARACTERISTICS: TERPERANCE/CORPUTER: PC CORCALION: END NO: 7125: SEQUENCE CHARACTERISTICS: TERPERANCE/CORPUTER: PC CORCALION: END NO: 7125: CORCALION: END NO:
00000000000000000000000000000000000000	RESULT 1 US-09-107-532A-7125 Sequence 7125, App. Sequence 7125, App. Fatent No. G58327 TITLE OF II INTILE OF

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; OTHER INFORMATION: Description of Artificial Sequence: GFP-HSC70 US-09-513-783A-174
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Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.3%; Score 44; DB 1; Length 646; 80.0%; Pred. No. 1.9;
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US-09-513-783A-174
US-09-513-783A-174

j Sequence 174. Application US/09513783A
j Patent No. 6416959
j GENERAL INFORMATION:
j APPLICANT: Giuliano, Kenneth A.;
j APPLICANT: Kapur, Ravi
j TITLE OF INVENTION: A System for Cell Based Screening
j TITLE OF INVENTION: A System for Cell Based Screening
j CURRENT APPLICATION NUMBER: US/09/513,783A
j CURRENT APPLICATION NUMBER: US/09/513,783A
j CURRENT PILING DATE: 2000-02-25
j NUMBER OF SEQ ID NOS: 180
j SSEQ ID NO 174
j LENGTH: 890
                                                                                                                                               COMPUTER TEACHER FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,139
FILING DATE: 15-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILO: Frank S.
REGISTRATION NUMBER: 31,3466
REGISTRATION NUMBER: 31,3466
                    E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/OCKET NUMBER: 8646
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEX: 210 901 SANS UR
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 646 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 86.3
Best Local Similarity 80.0
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        530 ŚLYEGIDFYT 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||:|||| ||
286 SLYEGIDFYT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SLFEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SLFEGIDIYT 10
CORRESPONDENCE ADDRESS:
                       ADDRESSEE: SCULLY,
STREET: 400 Garden
CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
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Sequence 3. Application US/08797358B

Patent No. 6268478

GENERAL INFORMATION:
APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN
NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
GITY: San Diego
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WEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OFBRATING SYSTEM: FC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFTCATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REFERENCE/DOCKET NUMBER: 31,815
REGISTRATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-9001
TELEPHONE: (619) 535-8049
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 643 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 46; DB 3; Length 643;
Pred. No. 0.8;
1; Mismatches 1; Indels
                                Length 226;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ), Anne S.
METHODS FOR INCREASING SECRETION OF RECOMBINANTLY EXPRESSED PROTEINS
20
                                                                            0; Indels
                                DB 4;
                                Score 46; DB 4;
Pred. No. 0.26;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDEDNESS: unknown TOPDLOGY: unknown MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-441-139-14

| Sequence 14, Application US/08441139
| Patent UN-05773245|
| Carberal INFORMATION: APPLICANT: Wittrup, Dr. Karl D. APPLICANT: Robinson, Anne S. TITLE OF INVENTION: METHODS FOR INC. TITLE OF INVENTION: RECOMBINANTLY FIGURAL PROPERTY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: California
COUNTRY: United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90.2%;
                                90.2%;
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Best Local Similarity 80.0
                Query Match
Best Local Similarity 88.,
8, Conservative
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                                                                                                                          2 LFEGIDIYT 10
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US-08-797-358B-3
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                                                                                                                                                                                                                Length 319;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,890A
FILING DATE: O'-UNN-1993
CLASSIFICATION - 435
PRIOR APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTONNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Klein, Michel
IITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                           68.6%; Score 35; DB 4; 75.0%; Pred. No. 48; Live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-466 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPRAX: (416) 595-1153
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: Sim & McBurney
6th Floor, 330 Unviersity Avenue
                                                                           , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...319
; SEQUENCE DESCRIPTION: SEQ ID NO: 6410:
US-09-107-532A-6410
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 19, Application US/08487890A Patent No. 5708149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: LOOSMOYE, Sheena
APPLICANT: Harkness, Robin
                                                                                                                                                                                                                                 Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                     126 LFQGIDIF 133
                                                                                                                                                                                                                                                                                                        2 LFEGIDIY 9
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CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6410, Application US/09107532A

Batent No. 6683275

GENERAL INFORMATION:
APPLICANT: Lynn: A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                 Sequence 532, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: ENTEROCOCCUS FARCALIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT FILING DATE: 1998-08-13
FILE REPERBYCE: 032796-032
CURRENT FILING DATE: 1998-08-13
FRIOR PELING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PATENTI VETSION 3.1
SEQ ID NO 5332
LIENGTH: 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-7un-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JULY 2, 1997
ATTORNEY_AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
COMPATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMPUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 6410:
SEQUENCE CHARACTERRISTICS:
LENGTH: 319 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: Enterococcus faecalis
US-09-134-000C-5332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:|:||::|
28 SIFDGIEVY 36
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Best Local Similarity
Matches 5; Conserv
         RESULT 5
US-09-134-000C-5332
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US-09-107-532A-6410
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Sequence 19, Application US/08337483 Patent No. 5922562 GENERAL INFORMATION:
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NAME: Stewart, Michael I

REGISTRATION NUMBER: 24,973

REFREENCE/DOCKET NUMBER: 1038-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
TOPOLOGY:
US-08-337-483-19
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                                                                                                                                                                                                                          USP-US-4/8-43-13-15
Sequence 19, Application US/08478435
Fatent No. 592223
Fatent No. 592223
FACENTAL INFORMATION:
PAPPLICANT: Chong, Pele
APPLICANT: GARY-Owen, Soott
APPLICANT: Murdin, Andrew
APPLICANT: Wan-Ping
APPLICANT: Wan-Ping
APPLICANT: Wan-Ping
APPLICANT: Wan-Ping
APPLICANT: Wan-Ping
APPLICANT: Wan-Ping
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APPLICANT: Wan-Ping
APPLICANT: Wan-Ping
APPLICANT: Wan-Ping
APPLICANT: Wan-Ping
CORRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
CITY: Toronto
CONNUTEX: Canada
STANE: Ontario
CONNUTEX: Toronto
CONUTEX: Toronto
CONUTEX: Toronto
CONUTEX: Toronto
CONUTEX: Toronto

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Matches 6; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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                                                 FEGIDIYT 10
                                                                                                  28 FEGVALYT 35
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RESULT 9 US-08-337-483-19

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Pred: No. 6.9;
1; Mismatches 1; Indels
                                                                                                                                                                                                                                GTREET: Suite 701, 330 Unviersity Avenue CITY: Toronto STATE: Ontario COUNTRY: Canada ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: ON TOWN ASSETT ON TOWN ASSET CLASSIFICATION: 435
ATTORNEY/AGENT INNORMATION:
NAME: Stewart, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Harkness, Robin
APPLICANT: Harkness, Robin
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Yang, Yan-Ping
APPLICANT: Mixflin, Andrew
APPLICANT: Mixflin, Andrew
APPLICANT: Mixflin, Andrew
APPLICANT: Trians (File)
APPLICANT: Mixflin, Andrew
APPLICANT: Trians (File)
TITLE OF INVENTION: Transferrin Receptor Genes
                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 Unviersity Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1038-410 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Suite CITY: Toronto STATE: Ontario
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; Sequence 19, Application US/08483577A
; Patent No. 6015688
; GENERAL INFORMATION:
; APPLICANT: Loosmore, Sheena
; APPLICANT: Harkness, Robin
; APPLICANT: Chong, Pele
; APPLICANT: Chong, Pele
; APPLICANT: Gray-Owen, Scott
APPLICANT: Wurdin, Andrew
; APPLICANT: Murdin, Andrew
; APPLICANT: Klein, Michel
; TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSE: Sim & McBurney
STREET: Suite 701, 330 Unviersity Avenue
CITY: Toxonto
CONTRESSE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,577A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/317,483
FILING DATE: 08-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; DB 3;
Pred. No. 6.9;
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                                           CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/337,483
FILING DATE: 08-NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/175,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/148,968
FILING DATE: 08-NOV-1993
ATTORNEY,AGENT INFORMATION:
NAME: SLEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-465 M
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
SEQUENCE CHARACTERISTICS:
TUNDAMINICATION AGINGS
     US/08/474,671
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 36 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acia
STRANDEDNESS: single
moboloGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 FEGIDIYT 10
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                            FILING DATE: 07
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY:
US-08-474-671-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
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Pred. No. 6.9;
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COMPUTER READABLE FORM:
MEDIUM TYES: Floppy disk
MEDIUM TYES: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE STRING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CLEASITICATION NUMBER: US/08/478,373
FILING DATE: 07-JUN-1995
FILING DATE: 08-NOV-1994
FILING DATE: 29-DEC-1993
FILING DATE: 29-DEC-1993
FILING DATE: 29-DEC-1993
FILING DATE: 29-DEC-1993
FILING DATE: 180-NOV-1993
FILING DATE: 180-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Locsmore, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Chong, Pele
APPLICANT: Chong, Pele
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Murdin, Andrew
APPLICANT: Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 147
CORRESPONDENGE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Suite 701, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1038-463 MIS:vg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 19, Application US/08474671; Patent No. 6008326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELEPHONE: (416) 595-1155
TELEPHONE: (416) 595-1163
INPORMATION POR SEQ ID NO: 19:
SEQUIENCE TELERACTERISTICS:
LENGTH: 36 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Toronto
STATE: Ontario
COUNTY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
COMPUTER: IRB PC COMP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 FEGIDIYT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: LOOSMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-478-373-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 11
US-08-474-671-19
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APPLICANT: LOSGONCE, Robin E
APPLICANT: Schrywers, Anthony B
APPLICANT: Chong, Pele
APPLICANT: Gray-Owen, Scott
APPLICANT: Wang, Yan-Ping
APPLICANT: Wang, Yan-Ping
APPLICANT: Klein, Michel H
TITLE OF INVENTION: HAEKOPHILUS TRANSFERRIN RECEPTOR GENES
CORRESPONDENCE: 147
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 4; Length 36;
Pred. No. 6.9;
                                                                                                                                                                                                                                                                                                                                     DB 3; Length 36;
                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE SIM & MCBULINGY
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Octanio
COUNTRY: Canada
ZID: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/637,654
FILLING DATE: 05-AUG-1996
                                                                                                                                                                                                                                                                                                                                     Score 34; DB 3
Pred. No. 6.9;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 05-AUG-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA94/00616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 19, Application US/08637654
Patent No. 6358727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
REGISTRATION NUMBER: 24,973
REPERBING/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1163
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 36 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36 amino acids
                                                                                                                                                                                     LENGTH: 36 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 75.0
Matches 6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                3 FEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 FEGVALYT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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Best Local Similarity
                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                             ;
TOPOLOGY:
US-08-897-438-19
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US-08-097-438-19
US-08-097-438-19
US-08-097-438-19
Sequence 19, Application US/08897438
Patent No. 6262016
GENERAL INFORMATION:
APPLICANT: Locamore, Sheena
APPLICANT: Acharyers, Robin
APPLICANT: Acharyers, Robin
APPLICANT: Andrew
APPLICANT: Wirdin, Michel
ITITLE OF INVENTION: Transferrin Receptor Genes
OCNRESSONDENCE ADDRESS:
ADDRESSES: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
COUNTY: Canada
CONFUTEN: IBM PC compatible
COMPUTEN: BATABALE FORM:
MEDIUM TYPE: BATABALE FORM:
COMPUTEN: BATABALE FORM:
MEDIUM TYPE: PATENTIN Release #1.0, Version #1.25
CUNFUTEN: DATE:
COMPUTEN: DATE:
COMPUTEN: BATABALE FORM:
APPLICATION NUMBER: US/08/897,438
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/483,577
PILING DATE: 09-001-093
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/15,116
FILING DATE: 29-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/15,116
FILING DATE: 09-001-093
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/15,116
FILING DATE: 09-001-093
ATTORNEY/AGENT INFORMATION:
NUMBER: US 08-001-093
ATTORNEY/AGENT INFORMATION:
NUMBER: SCHWALTION:
NUMBER: US 08-001-093
ATTORNEY/AGENT INFORMATION:
NUMBER: SCHWALT MICHAELI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
        FILING DATE: 29-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08 08/148,968

FILING DATE: 08-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Stewart, Michael 1

REGISTRATION NUMBER: 24,973

REFERENCE/DOCKET NUMBER: 1038-511

TELEPHONICATION INFORMATION:

SEQUENCE CHARACTERISTICS:

LENGTH: 36 anino acids

TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 75.0%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEGIDIYT 10
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           Gaps
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           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 6th FLOOI, 350 UNIVELEDY AVELLED
CTITY: TOTORIC
STATE: OLDEATIO
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER: ELADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/649,518
FLING DATE: 17-MAY-1996
CLASSIFICATION 536
FRID APPLICATION DATA:
APPLICATION NUMBER: US 08/483,577
FILING DATE: US 08/483,577
FILING DATE: US 08/175,116
FRICK APPLICATION NUMBER: US 08/175,116
FRICK APPLICATION UNBER: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: LOCOMOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Barkness, Robin
APPLICANT: Schryvers, Anthony
APPLICANT: Schryvers, Anthony
APPLICANT: Gray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Windin, Andrew
APPLICANT: Klein, Andrew
APPLICANT: Klein, Michel
TITLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: Geth Floor, 330 Unviersity Avenue
           ..
-i
     1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                              RESULT 15
US-08-649-518-19
'Sequence 19, Application US/08649518
'Pattent No. 6361779
6; Conservative
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                                                                                                           3 FEGIDIYT 10
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APPLICANT: LOOSMOI
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Search completed: September 15, 2004, 10:36:50 Job time : 16.7895 secs
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OM protein - protein search, using sw model

September 15, 2004, 10:29:20; Search time 53.1579 Seconds (without alignments) 53.153 Million cell updates/sec Run on:

Title: Perfect

US-09-673-795-2 51 1 SLFEGIDIYT 10 score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

1586107 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A_Geneseq_29Jan04:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp2004s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Aav44200 Heat	1 1	Heat	Human	1 DNA C	0 Hima	3 Human	9 Human	2 Human	2 Human	O Galline	CHOHOR 6	Firmar	Hilman	Himan		Himan	04 Mature	49 Filman h	Firman 2	34 Himan	f Human	11 Protes	ια	7 Mous
E .	AAY44200		AAB97603	ABR82812	ABM73781	AAY88410	AAY88413	AAY88409	AAY88412	AAB23252	AAR03930	AAR03929	AAW10065	AAY88408	AAY88411	AAB2365		AAR43004	AAW54349	AAB23652	AAB82534	AAE12986	ABU89711	ABR40398	ABR40397
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Abr40399	Abr40400	Add46498	Ade57092	Add45046	Add47457	Add47459	Ade76981	Aab23650	Abq93094	Abr52671	Abr52761	Aar03928	Abr40401	Abr40402	AAV44199	1946A	Abq79108	Adc97498	Abb71708
ABR40399	ABR40400	ADD46498	ADE57092	ADD45046	ADD47457	ADD47459	ADE76981	AAB23650	ABG93094	ABR52671	ABR52761	AAR03928	ABR40401	ABR40402	AAY44199	AAB97601	ABG79108	ADC97498	ABB71708
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47	47	47	47	47	47	47	47	47	47	47	47	47	47	47	46	46	46	46	46
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

Heat shock protein 70 amino acid residues 286-295. AAY44200 standard; peptide; 10 AA. 15-FEB-2000 (first entry) AAY44200;

Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HIA; immune defence; immunogenicity; specificity; human leucocyte antigen.

Homo sapiens

WO9954464-A1.

28-OCT-1999.

99WO-FR000957. 22-APR-1999; 98FR-00005033. 22-APR-1998;

(INSR) INST ROUSSY GUSTAVE.

Gaudin C; Triebel F, WPI; 2000-013251/01.

Identifying mutant peptides from heat-shock protein 70, for treatment of cancer.

Claim 10; Page 6; 56pp; French.

This peptide corresponds to amino acid residues 286-295 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce encoding DNA from one or more tumours; (ii) amplifying hsp70 sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer,

Sequence 10 AA;

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the amino acid sequence of fragment 2 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membrane. Recognition of increased numbers of HSP epitopes or cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen the pericellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or intracellular infected cells.
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particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumour-specific cytotoxic T lymphocytes in a cell culture and/or induce these calls to secrete cytotoxic factors (specifically interleukin-2, interferon-gamma and tumour necrosis factor), particularly where the cells are used to stimulate immune defences. The method identifies peptides with high immunogenicity and high specificity for particular HLA (human leucocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 2.
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                                                                                                                                                                                                                                  100.0%; Score 51, DB 3; Length 10; 100.0%; Pred. No. 0.00091; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB97602 standard; peptide; 10 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-2000; 2000WO-EP009530.
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                                                                                                                                                                                                                                                                            10; Conservative
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                                                                                                                                                          antigen) alleles
                                                                                                                                                                                                 Sequence 10 AA;
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the amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the pericellular membranes Recognition of increased numbers of HSPs piptopes or cell pericellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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                                                                                                                                                                                                                                                                                                                                         HSP, HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 3.
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100.0%; Score 51; DB 4; Length 10; 100.0%; Pred. No. 0.00091; ive 0; Mismatches 0; Indels
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Pred. No. 0.0062;
0; Mismatches 1; Indels
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                                   0; Mismatches
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                                                                                                                                                                                                   AAB97603 standard; peptide; 10 AA.
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                  ilarity 100.0%;
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Best Local Similarity
Matches 10; Conserv
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SLFEGIDEYT 10

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                                                                                                                                         Heat-shock protein 70; hsp70; antidiabetic; human; immunosuppressive;
dermatological; antiinflammatory; neuroprotective; antirheumatic;
antiarthritic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Pred. No. 0.014;
0; Mismatches 1; Indels
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                                                                                                             Human hsp70 peptide p20 (residues 286-305).
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                           ABR82812 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 33; 49pp; English.
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90.0%;
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                                                       ABR82812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diabetes.
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Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                        Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of barley varieties and production of barley transformants with desired
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90.0%; Pred. No. 0.45;
live 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID XX; 284pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY88410 standard; protein; 554 AA.
                                                                                                                                                               20-DEC-2001; 2001JP-00387131.
20-DEC-2001; 2001JP-00403299.
20-DEC-2001; 2001JP-00403309.
27-SEP-2002; 2002JP-00327815.
                                                                                                                                                                                                                                                                  Kohara Y;
                                                                                                                    16-DEC-2002; 2002WO-IB005403
                                                                                                                                                 2001JP-00387059
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Best Local Similarity 90.00,
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                                                                                                                                                                                                                                                                 Takeda K,
                             Hordeum vulgare
                                                        WO2003057877-A1
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20-DEC-2001;
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Sequence 554 AA;

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Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
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                                                                                                                               Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
                                                                                                                                                                                                             This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chromosome 1492-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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Pred. No. 0.58;
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                                                                                                                                                                                    Disclosure; Fig 3; 11pp; Japanese.
                                              (HOKE-) HOKEN KAGAKU KENKYUSHO KK
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                                                                                  2000-264458/23
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Best Local Similarity
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                                                                                                  N-PSDB; AAA15622
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Score 47; DB 3;
Pred. No. 0.58;
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0; Mismatches
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90.0%;
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Best Local Similarity
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Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
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                                                                                                                                                                                                                                                                                                                 This sequence represents the human heat shock protein SHSP70 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.
               Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; SHSP70.
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90.0%;
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                                                                                                                                                                                                                        WPI; 2000-264458/23.
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                                                                 sapiens
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Matches
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WPI; 2000-647056/62.

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The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a call which verexpresses Hsp72 (heat shock protein 71), and determining if the test compound inhibits activity or expression of Hsp72.

Conditionally, Hsp72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72—mediated JNK phosphatase of certivation, comprising ocntacting a test compound with a cell which expresses Hsp72, exposing the cell to a heat induced stress and determining if the compound inhibits JNK phosphatase activity. The invention additionally encompasses compositions comprising an inhibitor of Hsp72 or JNK phosphatase activity are useful for inhibiting the phosphatase or Hsp72 is used to treat a proliferative disorder such as carcinomas, breast cancer, prostate cancer). The compounds that inhibit msp72 is used to treat a proliferative disorder such as carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 function are administered to a patient compounds that inhibit Hsp72 function are administered to a patient compound that inhibit Hsp72 function are administered to a patient compound that inhibit Hsp72 function are administered to a patient compound that inhibit Hsp72 function are administered to a patient compound that inhibit Hsp72 function are administered to a patient carcuity relative to normal levels. The present sequence represents human Hsp72 used in the exemplifications of the invention
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                                   Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia, lymphoma.
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                                                                                                                 Example; Fig 16B; 77pp; English.
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Matches 9; Conserv
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Bacillus megaterium (Bmehsp70 - AAR03923); 3. E. coli (dnaK - AAR03924); 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus (rathsp70 - AAR03927); 7. Xenopus laevis (x170 - AAR03928); 8. Homo sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930); 10. Zea mays (mzehsp70 - AAR03931); 11. Serratia marcescens (smahsp70 - AAR03932). The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
AAY88408
                                                                                                                                                                                                                                                                                        RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              - used in
                                                                                                                   According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634. Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: 1. M. Myopneumoniae (Mhyhsp70 - AAR03922); 2. Bacillus megaterium (Bmehsp70 - AAR03923); 3. B. coli (dnaK - AAR03924); 4. T. cruzi (4c70kd - AAR03925); 5. T. cruzi (AAR03928); 6. Rat rattus (rathsp70 - AAR03929); 7. Kenopus laevis (x170 - AAR03928); 8. Homo sapiens (humhsp70 - AAR03929); 9. Gallus gallus (chkhsp70 - AAR03930); 11. Czea mays (meschsp70 - AAR0391); 11. Serratia marcescens (smahsp70 - AAR03923). The proteins having homology to hsp's of T. cruzi can be used in vaccines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                 Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proteins homologous to heat shock proteins of Trypanosoma cruzi - used vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.
                                                                                                                                                                                                                                                                                                                            Score 47; DB 2; Length 634;
Pred. No. 0.68;
                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 2.1-2.14; 86pp; English.
                                                                                                Disclosure; Fig 2.1-2.14; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR03929 standard; protein; 640 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88US-00243474.
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                                                                                                                                                                                                                                                                                                                                     92.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens HSP (humhsp70).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                  9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     289 SLFEGIDFYT 298
                                                                                                                                                                                                                                                                                                                                                                                           1 SLFEGIDIYT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Faulds D,
                                                                                                                                                                                                                                                                                Mycobacteria species
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                           WPI; 1990-115820/15
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Misc-difference
                                                                                                                                                                                                                                                                                                           Sequence 634 AA;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Detection of abnormal transcription of HSP70 mRNA - using HSP70 specific primer or probe, used in detection of human acute and chronic sustained stress load.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; heat shock protein 70; HSP70; primer; probe; detection; intracellular; abnormal transcription; acute; chronic; sustained; stress.
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                                                                        Score 47; DB 2; Length 640;
Pred. No. 0.69;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                     AAW10065 standard; protein; 640 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Fig 1; 13pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95JP-00158581
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                                                                           92.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
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                                                                                 Query Match
Best Local Similarity 90.0
Matches 9; Conservative
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Mycobacteria species
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Best Local Similarity
Matches 9; Conserv
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                                        Sequence 640 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-DEC-1996,
                                                                                                                                                                                                                                                                                                                                                                                                              24-OCT-1997
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95JP-00158581

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Search completed: September 15, 2004, 10:34:09 Job time : 54.6579 secs
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                                                                                                                                                                                                                                                                                                                     Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the human heat shock protein HSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                            Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
chromosome 14q22-24; transcription; rheumatism; schizophrenia;
depression; nephrotic syndrome; LHSP70.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92.2%; Score 47; DB 3; Length 640; 90.0%; Pred. No. 0.69; 1; Indels ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human heat shock protein LHSP70 amino acid sequence.
                                                                   Human heat shock protein HSP70 amino acid sequence.
AAY88408 standard; protein; 640 AA
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                                                                                                                                                                                                                                                                                                                                                           Claim 2; Fig 1; 11pp; Japanese.
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                                               (first entry)
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Matches 9; Conserv
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                                                                                                                                            Homo sapiens
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                                               31-JUL-2000
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                                                                                                   Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
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Pred. No. 0.69;
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(HOKE-) HOKEN KAGAKU KENKYUSHO KK
                                                                                                                                                                             Disclosure, Fig 4; 11pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92.2%;
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Best Local Similarity 90.00
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                                                     WPI; 2000-264458/23
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September 15, 2004, 10:30:46; Search time 32.6842 Seconds (without alignments) 86.882 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	O8:woodacdack	Ogue67 littoring n	Ogue70 littorina s	Oguese littoring a		1 _	٠.		Dalies animain	Ogoson oncorbinghii	Oggged firm mibrin	OSibms cetorbinis	O63718 vetting vett	ORiba4 nasadocerob	ORihan alonias sun	Ogjhsi alopias sup
	ID	O8UWM9	090667	090670	O9U669	Q9U665	O9U671	091666	0911668	D81159	090520	668860	ОВЛНИВ	063718	O8JHN4	OSCHEO	Q8JHS1
	DB	13	Ŋ	Ŋ	ഹ	Ŋ	Ŋ	Ŋ	Ŋ	Ŋ	13	13	13	Π	13	13	13
	Query Match Length DB	639	146	153	155	157	158	158	158	220	278	367	444	455	459	461	461
ою	Query	93.5	91.3	91.3	91.3	91.3	91,3	91.3	91.3	91,3	91.3	91.3	91.3	91.3	91.3	91.3	91.3
	Score	43	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42
	Result No.	П	7	m	4	ល	9	7	ω	σ	10	11	12	13	14	72	16

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QBJHP3 QBJHR2 QBJHR8 QBJHN3 QBJHR6	Q8JHP9 Q8JHQ7 Q8JHQ0 Q8JHP4 O8JHO3	Q8JHN1 Q8JHS9 Q8JHT4 Q8JHQ9	Q8JHT6 Q8JHR0 Q8JHS6 Q8JHD1 Q8JHD1 Q8JHS2	Q8JHS3 Q8JHN7 Q8JHT1 Q8JHR9 Q8JHR3	Q8JHT2 Q8JHP2 Q8JHS5 Q8JHN5
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ALIGNMENTS

RESULT 1 Q8UWM9

1 SLFEGIDIY 9

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Gaps

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Littorina scutulata (Checkered periwinkle).
Bukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
Littorinimorpha; Littorinoidea; Littorinidae; Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Littorina plena (Black periwinkle).

Bukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Heat-shock genes in the heat-stressed genus Littorina.";
submitted (oCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AF191826; AAF12785.1; -.
GO, GO:000524; FATP binding; IRA.
InterPro; IPR001023; HSp70.
PEROM; PD000089; HSp70; 1.
PROSITE; PS01036; HSP70.3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Hear-shock genes in the hear-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL; AF191830; AAF12789.1; -.
GO; GO:0005524; F.ATP binding; IEA.
InterPro; IPR001023; HSp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 155;
      91.3%; Score 42; DB 5; Length 153; 88.9%; Pred. No. 1.8; ive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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155 155
155 AA; 17676 MW; C191F6E5B1F346C2 CRC64;
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1.MAY-2000 (TrEMBLrel. 13, Last sequence update)
01.0CT-2003 (TrEMBLrel. 25, Last annotation update)
Heat-shock protein (Fragment).
                                                                                                                                                                                                                                                                            01-NAY-2000 (TrEMBLrel. 13, Created)
01-NAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
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Pred. No. 1.8;
0; Mismatches 1
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                                                                                                                                                                                                                                           155 AA
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                                                                                                                                                                                                                                                                                                                                              Heat-shock protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.3%;
88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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             Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                       80 SLFEGIDFY 88
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                                                                                             1 SLFEGIDIY
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SEQUENCE
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Q9U665;
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                                                                                                                                                                                                      RESULT
Q9U669
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                                                                                                                                                                                                                                                Littorina plena (Black periwinkle).
Bukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Carogastropoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
submitted (CCT-1999) to the BMBL/GenBank/DDBJ databases.
-! SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AF191828; AAF12787.1; -.
GO; GO:005524; F:ATP binding; IEA.
InterPro; IPR001023; HSP70.
PFam; PF00112; HSP70.
PROSITE; PS01036; HSP70; 1.
PROSITE; PS01036; HSP70; 3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           91.3%; Score 42; DB 5; Length 146; 88.9%; Pred. No. 1.7; Live 0; Mismatches 1; Indels
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153 153
153 AA; 17352 MW; E29EE20C4CAF934D CRC64;
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16607 MW; C3F3556A1AF438BB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                     090667;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat-shock protein (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Littorina scutulata (Checkered periwinkle).
                                                                                                      146 AA
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                                                                                                      PRELIMINARY;
288 SLFEGVDLY 296
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                                                   Hohenlohe P.A.;
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Q9U668;
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Q9U668
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Eukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda, Sorbeoconcha, Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
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Littorina plena (Black periwinkle).

Bukaryots, Metazoa, Mollusca, Gastropoda; Orthogastropoda;

Apogastropoda, Caenogastropoda, Sorbeoconcha; Hypsogastropoda,

Littorinimorpha; Littorinoidea; Littorinidae; Littorina.

NCBI_TaxID=31219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hohenlohe P.A.;
"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                         91.3%; Score 42; DB 5; Length 157; 88.9%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91.3%; Score 42; DB 5; Length 158; 88.9%; Pred. No. 1.8;
                                                                                                                                                                                                                     1; Indels
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                                                                                              157 157
157 AA; 17834 MW; B8F743382B2BBB2 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat-shock protein (Fragment).
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InterPro; IPR001023; Hsp70.
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Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HBATSHOCK70.
ProDom; PD000089; HSP70; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding.
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NOW_TER 157 157
SEQUENCE 157 AA; 17834 MW; 1
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PRINTS; PR00301; HSP70; 1.
ProDom; P000089; HSP70; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding. 1
NON TER 1
NON TER 158 SEQUENCE 158 AA; 17887 WW; 1
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Best Local Similarity 88.
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Best Local Similarity
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Q9U671
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Bukaryota, Metazoa, Mollusca, Gastropoda, Orthogastropoda,
Apogastropoda, Caenogastropoda; Sorbecconcha; Hypsogastropoda,
Littorinimorpha, Littorinoidea, Littorinidae, Littorina.
WCBI_TaxID=31219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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"Heat-shock genes in the heat-stressed genus Littorina.";
Submitted (oct-1999) to the BMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
SON GO:0005224; F.ATP binding; IEA.
InterPro; PR001023; HSP70.
Pfam: PF000123; HSP70.
PRINTS; PR00101; HSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.3%; Score 42; DB 5; Length 158; 88.9%; Pred. No. 1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    158 AA; 17891 MW; B41E5356BCECAD2F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158 AA; 17868 MW; D2ECE71042EC44CB CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91.3%; Score 42; DB 5; ilarity 88.9%; Pred. No. 1.8; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           220 AA.
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PROSITE; PS01036; HSP70_3; 1.
ATP-binding.
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PROSITE; PS01036; HSP70_3; 1.
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                                                                       Eŭkāryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
Apogastropoda; Heterobranchia; Euthyneura; Opisthobranchia; Anaspidea;
                                                                                                                                                      Kuhl D., Kennedy T., Barzilai A., Kandel E.;
Kuhl D., Kennedy T., Barzilai A., Kandel E.;
"Long-term sensitization training in Aplysia leads to an increase in the expression of Blp, the major protein chaperon of the ER.";
J. Cell Biol. 119:1069-1076 (1922).
-i. INDUCTION: CONSTITUTIELY SYNTHESIZED IN A WIDE VARIETY OF CELLS.
-i. SIMILARITY: BELONGS TO HEAT SHOCK PROTEIN 70 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 05, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Rainbow trout 70 KDa heat shock protein (Fragment).
Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
Actinopterygii, Metzoza, Chordata, Cramitata, Vertebrata; Euteleostomi;
Actinopterygii, Neopterygii; Teleostei; Buteleostei;
Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X MEDLINE=85036330; PubMed=6092938; MEDLINE=85036330; PubMed=6092938; MEDLINE=85036330; PubMed=6092938; A Kothary R.K., Jones D., Candido E.P.M.; "70-kilodalton heat shock polypeptides from rainbow trout: Tharacterization of cDNA sequences."; Mol. Cell. Biol. 4:1785-1791(1984). ". Mol. Cell. Biol. 4:1785-1791(1984). ". EMBL; K02549; AAA49562.1; -. SIMILARIYY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY. EMBL; K02549; F.AFP binding; IEA. RSSP; P08107; IHJO. GO; GO:0005524; F.AFP binding; IEA. GO; GO:000573; F.AFP binding; IEA. InterPro; IPR001023; HSP70. R PÉm; PR00012; HSP70. R PÉm; PR00012; HSP70; I. R PRINTS; PR00311; HEATSHOCK770. R PODD: PD000089; HSP70; I. R PROSITE; PS00329; HSP70. 2: 1.
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Pred. No. 2.6;
0; Mismatches 1; Indels
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EMEL; Z15039; CAA78757.1; -
PIR; B44261; B44261;
F184261; B44261;
G0; G003773; F: heat shock protein activity; IEA.
Interpro; IPR001023; H8p70.
PFEM; PF00012; H8p70; 1.
PROSITE; PS00329; H8p70; 1.
PROSITE; PS01036; H8p70; 1.
 01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-JUN-2003 (TrEMBLrel. 24, Last annotation update) Heat shock cognate 71 kDa protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          278 AA.
                                                          Aplysia californica (California sea hare).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                              Aplysioidea; Aplysiidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 SLFEGIDFY 146
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                                                                                                                                              SEQUENCE FROM N.A.
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Wataryotes, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes;
Blasmobranchii, Galeomorphii, Galeoidea, Lammiformes, Alopiidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei; Acanthomorpha; Acanthopororpha; Percomorpha; Tetraodontiformes; Tetraodontoidea; Tetraodontidae; Takifugu.
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                                                                                        Length 278;
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                                                                                                                              Indels
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                                   278
30327 MW; E4C745DE5484C17A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Habs; F1912.0. SHOWN GO), GO: 0006524; F:ATP binding; IEA.
GO; GO:0003773; F:heat shock protein activity; IEA.
InterPro; IFR001023; Hsp70.
PRO012; HSP70; 2.
PRINTS, PR00121; HEATSHOCK70.
ProDom; PD0000089; Hsp70; 1.
PROSITE; PS01036; HSP70; 1.
PROSITE; PS01036; HSP70; 3:
ATP-binding; Heat shock.
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                       01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
70kD heat shock protein (Fragment).
                                                                                        Score 42; DB 13;
Pred. No. 3.4;
0; Mismatches 1.
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                                                                                                                                                                                                                                                                                                      367 AA
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                                                                                            91.3%;
88.9%;
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01-0CT-2002 (TrEMBLrel. 22,
01-0CT-2003 (TrEMBLrel. 25,
                                                                         Query Match
Query Match
Best Local Similarity 88.5°,
Best Local Similarity
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ATP-binding; Heat shock.

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SEQÜENCE 278 AA; 3032
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Best Local Similarity
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Cetorhinus

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1 SLFEGIDIY 9
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                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=57991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=57980;
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                                                                                               Q8JHN4
Q8JHN4;
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QBJHS0
                                                      RESULT 14
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                                                                            08JHN4
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                        Marrin A.P., Burg T., "Perils of paralogy: Using Hsp70 genes for inferring organismal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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88.9%; Pred. No. 5.6;
active 0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               444 AA; 48889 MW; 7701945FBB99A2BA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Heat shock rotein 70 (Fragment).
Rattus rattus (Black rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005524; F:ATP binding; IEA.
InterPro; IPR001023; Hsp70.
Ffam: PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHCKTO.
PROSITE; PS00329; Hsp70; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
                                                                                                                                                                                                                                                                                                                PRINTS; PRO0301; HEAYSHOCK70.
PRODOM; PD000089; HSP70; 1.
PROSITE; PS00329; HSP70-2; 1.
PROSITE; PS01036; HSP70-3; 1.
ATP-binding.

NON_TER
SEQUENCE 444 AA, 48889 MW; 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               247 SLFEGIDFY 255
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                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                     NCBI_TaxID=57982;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4
4
55
                                                                                          STRAIN=Cema6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        063718;
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Q63718
DG Q63711
DG O1-NO'
DT O1-NO'
DT O1-NO'
DT O1-NO'
DE Heat 19
OS Bukatu
OC Bukatu
OC Mamma
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OC Mamma
CC M
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Gaps

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254 SLFEGIDFY 262

1 SLFEGIDIY 9

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Gaps
                                                                                                                Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Chondrichthyes,
Elasmobranchii, Galeomorphii, Galeoidea, Lamniformes,
Pseudocarchariidae, Pseudocarcharias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alopias superciliosus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
Elasmobranchii; Galeomorphii; Galeoidea; Lamniformes; Alopiidae;
                                                                                                                                                                                                    STRAIN=Pska5;
Martin A.D., Burg T.;
"Perils of paralogy: Using Hsp70 genes for inferring organismal
                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Perils of paralogy: Using Hsp70 genes for inferring organismal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             phylogenies.";
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
EMBL, AFF02452; AAM5160.1; -.
GO: GO: 0005524; FATP binding; IEA.
InterPro; IPR01023; Hsp70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.3%; Score 42; DB 13; Length 459; 88.9%; Pred. No. 5.8; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       459 459
459 AA; 50209 MW; 0D0055A45248652A CRC64;
                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
   459 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   461 AA.
                            Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
   PRT;
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                         01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2002 (TrEMBLrel. 22, 01-0CT-2003 (TrEMBLrel. 25, HSp70 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2002 (TrEMBLrel, 22, 01-0CT-2002 (TrEMBLrel, 22, 01-0CT-2003 (TrEMBLrel, 25, HSp70 protein (Fragment).
                                                                                                  Pseudocarcharias kamoharai.
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity 88.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SLFEGIDFY 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Martin A.P., Burg T.;
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DR Probom; PD000089; Hsp70; 1.

DR PROSITE; PS01036; HSP70_2; 1.

DR ATP-binding.
FT NOW_TER 461 A61

SQ SEQUENCE 461 AA; 50591 MW; 1A9ESB4EC41077FE CRC64;

Query Match

Best Local Similarity 88.9%; Pred. No. 5.8;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps

Qy 1 SLFEGIDIY 9

Db 246 SLFEGIDY 254

Search completed: September 15, 2004, 10:35:44

JOB time : 33.6842 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

September 15, 2004, 10:30:21; Search time 8.05263 Seconds (without alignments) 58.196 Million cell updates/sec Run on:

US-09-673-795-1 46 1 SLFEGIDIY 9

Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

141681 seqs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seg length: 0 Maximum DB seg length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt 42:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

0

420 AA.

PRT;

STANDARD;

RESULT 2 HS1A MOUSE ID HS1A MOUSE

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41 89.1 648 1 HS71 PUCCR PP5503 Tattus nory 85 8 94.8 641 HS71 PUCCR PP5503 Tattus nory 85 8 94.8 641 HS71 PUCCR PP5503 Tattus nory 85 8 94.8 641 HS72 PUCNN PP4991 homo sapien nory 85 9 94.8 641 HS72 PUCNN PP4991 PP5503 Tattus nory 85 9 94.8 641 HS72 PUCNN PP4991 PP5503 Tattus nory 99 9 9 94.8 642 HS 642 HS72 PUCNN PP4991 PP5503 PP5491 PP5603 PP5
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HS71 PUCGR HS74 HUMAN HS71 SCHPO HS71 SCHPO HS71 SCHPO HS71 SCHPO HS71 SCHPO HS72 LYCES HS70 SOYEN HS72 LYCES HS70 SOYEN HS72 LYCES HS70 SOYEN HS72 LYCES HS70 SOYEN HS72 LYCES HS70 SOYEN HS72 LYCES HS70 SOYEN HS72 LYCES HS70 SOYEN
1 HE HE HE HE HE HE HE HE HE HE HE HE HE
41 89.1 648 1 HS71_PUCGR
4 41 89.1 648 5 39 84.8 641 8 39 84.8 641 8 39 84.8 642 9 39 84.8 644 2 39 84.8 644 2 39 84.8 645 2 39 84.8 645 2 39 84.8 646 5 39 84.8 646 5 39 84.8 646 5 39 84.8 646 5 39 84.8 646 5 39 84.8 646 5 39 84.8 646 5 39 84.8 646 5 39 84.8 646 5 39 84.8 646 5 39 84.8 18 646 5 30 84.8 646 6 466 6 466 6 40 866
34 41 89.1 35 39 84.8 36 39 84.8 37 39 84.8 38 39 84.8 39 84.8 39 84.8 39 84.8 40 39 84.8 41 39 84.8 42 39 84.8 44 39 84.8 45 39 84.8 45 39 84.8 46 39 84.8 47 39 84.8 48 39 84.8 49 39 84.8 49 39 84.8 40 1-671-199 (Rel. 10-671-199 (Rel. 11-7AR-2004 (Rel. 15-MAR-2004 (Rel. 15-MAR-2004 (Rel. 15-MAR-2004 (Rel. 16-MAR-2004
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RESTANTED SOCIETARY SERVICES COURSES AND SOCIETARY SERVICES COURSES CO

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heat shock 70 kDa protein (HSP70).
Gallus gallus (Chicken).
Eukaryota, Metazoa, Chadta, Craniata, Vertebrata, Euteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Morimoto R.I., Hunt C., Huang S.-Y., Berg K.L., Banerji S.S., "Organization, nucleotide sequence, and transcription of the chicken HSP70 gene.";
                                                                                                                                                                                                                                                                                                                                                                                                  Shen H.D., Au L.C., Lin W.L., Liaw S.F., Tsai J.J., Han S.H., Molecular cloning and expression of a Penicillium citrinum allergen with sequence homology and antigenic crossreactivity to a hsp 70
                                                                                                                                                                                                         Bukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Burotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biol. Chem. 261:12692-12699(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Exp. Allergy 27:682-690(1997).
-!- ALLERGEN: Causes an allergic reaction in human.
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
                16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Heat shock 70 kDa protein (Allergen Pen c 19) (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 AA; 55125 MW; B7433C11FAEA1320 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91.3%; Score 42; DB 1;
88.9%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATP-binding; Chaperone; Heat shock; Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     634 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLODOM; PD000089; HSP70; I. PARTIAL. PROSITE; PS00292; HSP70_1; PARTIAL. PROSITE; PS00329; HSP70_2; I. PROSITE; PS01036; HSP70_3; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=86304452; Pubmed=3017985;
                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97351908; PubMed=9208190;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U64207; AAB06397.1; -.
HSSP; P19120; 3HSC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human heat shock protein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          154 SLFEGIDFY 162
                                                                                                                                                                                  Penicillium citrinum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SLFEGIDIY 9
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Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                              NCBI_TaxID=5077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 4
HS70 CHICK
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SOLUTION NEW TRANSPORTED TO THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF THE SECOND OF TH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Provides a properation with other chaperones, Hsp70s stabilize preexistent proteins against aggregation and mediate the folding of newly translated polypeptides in the cytosol as well as within organelles. These chaperones participate in all these processes through their ability to recognize nonnative conformations of other proteins. They bind extended peptide segments with a net hydrophobic character exposed by polypeptides during translation and membrane translocation, or following stress-induced damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=86111900; PubMed=2868009;
Lowe D.G., Moran L.A.;
"Molecular cloning and analysis of DNA complementary to three mouse mar = 68,000 heat shock protein mRNAs.";
J. Biol. Chem. 261:2102-2112(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perry M.D., Aujame L., Shtang S., Moran L.A.; "Structure and expression of an inducible HSP70-encoding gene from
                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1011_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                           01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Heat shock protein 1A (Heat shock 70 kDa protein 3) (HSP70.3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42; DB 1; Length 420; Pred. No. 0.93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M12571; AAA57234.1; -.
EMBL; M12572; AAA57235.1; -.
EMBL; M2572; AAA57235.1; -.
EMBL; M26283; AGC83.
HSSP; P08109; 1CKR.
MGD; MGI:96244; Hspala.
InterPro; IPR00123; Hsp70.
Pfam; PF00012; HSP70; 1.
PRINTS; PR00301; HSP70; 1.
PROSITE; PS00297; HSP70 1; PARTIAL.
PROSITE; PS01036; HSP70 2; PARTIAL.
PROSITE; PS01036; HSP70 3; 1.
PROSITE; PS01036; HSP70 3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46292 MW; 5DA1C6155C7B16B5 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V -> G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 155-420 FROM N.A.
MEDLINE=94357449; PubMed=8076831;
                                       Created)
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                                                                                                                                                                                  (Figurenc):
HSPA1A OR HSP70-3 OR HSP70A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus.";
Gene 146:273-278(1994).
                                 01-NOV-1997 (Rel. 35,
01-NOV-1997 (Rel. 35,
10-OCT-2003 (Rel. 42,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73
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420 AA;
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      061696; 061697;
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HS70_PENCI
ID HS70_PENCI
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STTTS BRANK

SEQUENCE Query Match

Matches Best

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VARITANT

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Gaps

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Length 503; Indels

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"The hec70 gene which is slightly induced by heat is the main virus
inducible member of the hsp70 gene family.";

"The hec70 gene which is slightly induced by heat is the main virus
inducible member of the hsp70 gene family.";

"EBSE Lett. 355:282-286(1994).

"I FEBS Lett. 355:282-286(1994).

"I FEBS Lett. 355:282-286(1994).

"ORANELISTERNY PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING
OF NEWLY TRANSLATED POLYPEPTIDES IN THE SYNOPLASMIC
OF RETICULOM PLAX AN ADDITIONAL ROLE BY PROVINING A DELYING FORCE FOR
RETICULOM PLAX AN ADDITIONAL ROLE BY PROVINING A DELYING FORCE FOR PROTEIN TRANSLOCATION. THEY ARE INVOLVED IN SIGHAL TRANSDUCTION
PROFESSES THROUGH PLAY ARE INVOLVED IN SIGHAL TRANSDUCTION
PROCESSES THROUGH PLAY REILINY TO RECOGNIZE NONNATIVE
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES
SEGMENTS WITH A NET HYDROPHOBIC CHARACTER EXPOSED BY POLYPERTIDES
CONFORMATIONS OF OTHER PROTEINS. THEY BIND EXTENDED PEPTIDES
STRESS-INDUCED DAMAGE.

"INDUCTION: By heat shock."

"INDUCTION: By heat shock."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
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                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00012; HSF/U; 1.

PRINTS; PR00301; HBATSHOCK70.

PROSITE; PS00299; HSP70; 1.

PROSITE; PS00329; HSP70; 1.

PROSITE; PS01036; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Heat shock; Multigene family.

ATP-binding; Heat shock; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecus aethiops (Green monkey) (Grivet),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
ieat shock 70 kbg protein 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                  EMBL; J02579; AAA48825.1; -. PIR; A25646; A25646.
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InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
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les 8; Conserv
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15-DEC-1998
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1D H871_CERAE

1D H871_CERAE

DT 15-DEC-:

DT 15-DEC-:

DE Heat bEAD-IN-

GN HSPA1.

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STRAINS-2888C / AB972;
WEDLINE-97313267; PubMed-9169871;
WEDLINE-97313267; PubMed-9169871;
WEDLINE-97313267; PubMed-9169871;
A Donston M., Hiller L., Riles L., Albermann K., Andre B., Ansorge W., Benes V., Brueckner M., Osffeau A., Hebling U., Heumann K., Huss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis B.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Scholler P., Schwarz S., Scholler P., Schwarz S., Scholler P., Schwarz S., Underwood A.P., Urrestarazu L.A., Vandenboll M., Verhassell F., Voet M., Volckaert G., Voss H., Wambutt R., Wedler E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
"The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.",
                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The sequence of 32kb on the left arm of yeast chromosome XII reveal
six known genes, a new member of the seripauperins family and a new
ABC transporter homologous to the human multidrug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Slater M.R., Craig E.A., "The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae."; Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast),
Eukaryota; Fungi; Ascomycota; Saccharomycetes;
                                                                                                                                                                                                                                                                                  .
0
                                                                                                                                                                                                                                             Score 42; DB 1; Length 638;
Pred. No. 1.4;
0; Mismatches 1; Indels
                                                                                                                                                                                              shock; Multigene family.; D55076A0FFAB6AB3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-JUL-1989 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=8288C;
MEDLINE=89128457; PubMed=2644626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=5288c;
MEDLINE=97197984; PubMed=9046100;
                                                         HSSP, P08107, 110.

InterPro; IPR001023; Hsp70.

Fam, PP00012; HSP70, 1.

PRINTS; PR00301; HEATSHOCK70.

PROSITE; PS00297; HSP70, 1.

PROSITE; PS00297; HSP70_1; 1.

PROSITE; PS01036; HSP70_2; 1.

PROSITE; PS01036; HSP70_3; 1.

ATP-binding; Chaperone; Heat sho SEQUENCE 638 AA; 69920 MW; D
                                                                                                                                                                                                                                                                             . 0
                                                                                                                                                                                                                                             91.3%;
88.9%;
                              EMBL; X70684; CAA50019.1;
PIR; S31766; S31766.
                                                                                                                                                                                                                                                                             8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          shock protein SSA2.
OR YLL024C OR L0931
                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Purnelle B., Goffeau A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Teast 13:183-188(1997),
                                                                                                                                                                                                                                                                                                                                              284 SLFEGIDFY 292
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Best Local Similarity
Matches 8; Conserv
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HS72 YEAST
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SEQUENCE OF 91-97 AND 325-341.

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STANDARD;
                     STANDARD;
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                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Paracentrotus
                   HS71 ORYLA
Q918F9;
28-FEB-2003 (
28-FEB-2003 (
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Q06248;
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HS74_PARLI
HS71_ORYLA
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                                                                                                                                                                                                             "Protein expression during exponential growth in 0.7 M NaCl medium of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                      Garrals J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
Submitted (SEP-1994) to Swiss-Prot.
-!- FUNCTION: SSA2 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE STOPLASMATIC RETICULIN. A FUNCTIONAL DIPFERENCE BETWEEN YEAST SNAL AND SSA2 PROFIEDS. SKA2CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
       MEDLINE=95203288; PubMed=7895733;
Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender E Volge T., Warner J.R., McLaughlin C.S.;
"Protein identifications for a Saccharomyces cerevisiae protein database.";
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- PTM: Phosphorylated.
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 1; Length 638;
Pred. No. 1.4;
0; Mismatches 1; Indels
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GO; GO:0005737; C:cytoplasm; IDA.
GO; GO:0000329; C:vacuolar membrane (sensu Fungi); IDA.
GO; GO:0003773; P:heat shock protein activity; IMP.
InterPro; IPR001023; Hsp70.
InterPro; IPR00123; Hsp70.
InterPro; IPR00123; Hsp70.
InterPro; IPR00124; Hsp70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PRO0301; HEATSHOCK70.
PRODOM; PD000089; HSP70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00309; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
Heat shock; AIP-binding; Multigene family; Acetylation; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACETYLATION.
23BDDD120C194912 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Cytoplasmic.
                                                                                                                                                                                                                                       Saccharomyces cerevisiae.";
FEMS Microbiol. Lett. 137:1-8(1996).
                                                                                                  Electrophoresis 15:1466-1486(1994).
                                                                                                                                                          STRAIN=ATCC 38531 / Y41;
MEDLINE=97089742; PubMed=8935650;
                                                                                                                                                                                                                                                                                               ACETYLATION, AND PHOSPHORYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; X12927; CAA31394.1; -...
EMBL; Z73129; CAA97472.1; -...
EMBL; X9760; CAA66167.1; -...
PIR, S20139; S20139.
HSSP; P19120; 3HSC.
GermOnline; 142019; -...
SWISS-2DPAGE; P10592; YEAST.
COMPLUYEAST-2DPAGE; P10592; -...
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88.9%;
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Best Local Similarity 88.5.,
8; Conservative
                                                                                                                                                                                                   Norbeck J., Blomberg A.;
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                                                                                                                                              SEQUENCE OF 186-195.
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                                         28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amnotation update)
28-FEB-2003 (Rel. 41, Last amnotation update)
28-FEB-2003 (Rel. 41, Last amnotation update)
28-FEB-2003 (Rel. 41, Last amnotation update)
Coryzias latipes (Medaka fish) (Japanese ricefish).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzinas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [1] — SEQUENCE FROM N.A. MEDINE-930775; Sconzo G., Scardina G., Ferraro M.G.; Sconzo G., Scardina G., Ferraro M.G.; Sconzo G., Scardina of a new member of the sea urchin Paracentrotus "Characterization of a new member of the sea urchin Paracentrotus lividus hap70 gene family and its expression."; Gene 121:553-358(1992). i- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .;
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                                                                                                                                                                                                                                                                                                                                                                                           Naruse K., Sakuragi M.;
"Medaka HSP70 gene cloning.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
-i- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 1; Length 639;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prodom; PD000089; HSp70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01329; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 639 AA; 70350 MW; 610B7E0DC0EB0534 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
Heat shock 70 kDa protein IV (HSP70 IV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      639 AA
639 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF286875; AAF91485.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR01023; Hsp70.
Pfam; PP00012; HSP70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=88297155; PubMed=2841196;
Snutch T.P., Heschl M.F.P., Baillie D.L.;
"The Caenorhabditis elegans hsp70 gene family: a molecular genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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-!- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          91.3%; Score 42; DB 1; Length 639; 88.9%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                               HSSP, P19120, 3HSC.

InterPro: IPR001023; HSp70.

Pfam; PP00012; HSP70.

PRONTS: PR00101; HSP70.

PRODOM; PD000089; HSP70; 1.

PROSITE; PS00239; HSP70 1; 1.

PROSITE; PS01329; HSP70 2; 1.

PROSITE; PS01036; HSP70 3; 1.

PROSITE; PS01036; HSP70 3; 1.

PROSITE; PS01036; HSP70 3; 1.

ATP-binding; Heat shock; Multigene family.

SEQUENCE 639 AA; 69749 MW; 40E2F29570806DCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Prodom; PD000089; Hsp70; 1.
PROSTTE; PS00297; HSP70_1; 1.
PROSTTE; PS00329; HSP70_2; 1.
PROSTTE; PS01036; HSP70_3; 1.
ATP-binding; Heat shock; Multigene family.
SEQUENCE 640 AA; 69823 MW; ED15409D06C500C2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
Heat shock 70 kDa protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       640 AA
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0; Mismatches
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InterPro; 1PR001023; HSp70.
Pfam; PF00012; HSp70; 1.
PRINTS; PR00301; HEATSHOCK70.
                                                                                                                                                                                                                                                       EMBL; X61379; CAA43653.1; -. PIR; JC1391; JC1391.
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PIR; JT0285; HHKW7A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  286 SLFEGIDFY 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SLFEGIDIY 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Local 8; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         characterization.
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H87A_CAREL

AC P09446;
DT 01-MAR-1989
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MEDLINE=94043116; PubMed=8226849;

MEDLINE=94043116; PubMed=822684;

MEDLINE=9404316; PubMed=82268;

MEDLINE=940416; PubMed=940416;

MEDLINE=940416;

MEDLINE
                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Haus U., Trommler P., Fisher P.R., Hartmann H., Lottspeich F., Noegel A.A., Schleicher M.; "The heat shock cognate protein from Dictyostelium affects actin polymerization through interaction with the actin-binding protein
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SEQUENCE FROM N.A., AND SEQUENCE OF 34-46; 102-106 AND 298-309.
                     Length 640;
                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Mycetozoa; Dictyostellida; Dictyostellum.
NCBI_TaxID=44689;
        91.3%; Score 42; DB 1;
88.9%; Pred. No. 1.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
15-WAR-2004 (Rel. 43, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       640 AA
                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heat shock cognate protein (Aginactin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
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SWISS-2DPAGE; P36415; DICTY.
DictyBase; DDB0001837; hspB.
InterPro; IPR001023; Hsp70.
PRINTS; PR00301; HSATSHOCK70.
PRODOM; P000089; Hsp70; 1.
PROSITE; PS00297; HSP70; 1.
PROSITE; PS00297; HSP70; 1.
PROSITE; PS00329; HSP70-2; 1.
PROSITE; PS01036; HSP70-2; 1.
ATP-binding; Chaperone.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBO J. 12:3763-3771(1993).
Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD:
                                                                                                                                                                                                                                                  287 SLFEGIDFY 295
                                                                                                                                                                     1 SLFEGIDIY 9
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P36415;
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AC H87C_DICDI

DT H87C_DICDI

DT 15-MAN

DE Heat 60

ON HSPB 01

ON HSB 
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PIR; S53357; S53357.
                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                 Gutierrez J.A., Guerriero V.; "Chemical modifications of a recombinant bovine stress-inducible 70 KDa heat-shock protein (Hsp70) mimics Hsp70 isoforms from tissues."; Biochem. J. 305:197-203 (1995).
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Angus;
MEDLINE=95030563; PubMed=7943958;
Grosz M.D., Skow L.C., Stone R.T.;
"An Alui polymorphism at the bovine 70 kD heat-shock protein-1
                                                                                                   . 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRESS-INDUCED DAMAGE.
INDUCTION: By heat shock.
SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                91.3%; Score 42; DB 1; Length 640; 88.9%; Pred. No. 1.4;
                                                                                                    Indels
N -> T (IN REF. 2).

R -> A (IN REF. 2).

R -> A (IN REF. 2).

S -> A (IN REF. 2).

V -> A (IN REF. 2).

V -> D (IN REF. 2).

F -> P (IN REF. 2).

ZEGBDC2DB96A9FSD CRC64;
                                                                                                    1;
                                                                                                                                                                 HS71 BOVIN

HS71 BOVIN

C HS71 BOVIN

AC C 27975; 027964;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1999 (Rel. 38, Last sequence update)

DT 15-UUL-1999 (Rel. 38, Last sequence update)

DT 15-UUL-1999 (Rel. 38, Last annotation update)

DE Heat shock 70 kDa protein 1 (HSP70-1).
                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                 [1]
SEQUENCE FROM N.A.
TISSUB-Skeletal muscle;
MEDLINE-95126904; PubMed-726329;
                                                                                                    ;
  Z > Z S S > H F
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 212-641 FROM N.A.
                                                                 70499 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U09861; AAA73914.1; -. EMBL; U02891; AAA03450.1; -.
                                                                                                     8; Conservative
   32
64
233
341
352
                                                                                                                                       SLFEGIÓFY 292
                                                                                                                      1 SLFEGIDIY 9
                                                                                                                                                                                                                                                  Bos taurus (Bovine)
                                                                 640 AA;
                                                                                          Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                    NCBI_TaxID=9913;
    32
64
180
237
240
352
          CONFLICT
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TISSUB-Muscle, Parcreas, and Skin;
MEDLINE=22388257; PubWed=12477932;
Straubberg R.L., Feingrold E.A., Grouse L.H., Derge J.G.,
Straubberg R.L., Collins F.S., Wagner L., Shennen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.L., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
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Shiina S., Tamiya G., Oka A., Inoko H.;
"Homo sapiens 2,229,817bp genomic DNA of 6p21.3 HLA class I region.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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MEDLINE=66016721; PubMed=3931075;
Hunt C., Morimoto R.I.;
"Conserved features of eukaryotic hsp70 genes revealed by comparison with the nucleotide sequence of human hsp70.";
Proc. Natl. Acad. Sci. U.S.A. 82:6455-6459(1985).
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Milner C.M., Campbell R.D.; "Structure and expression of the three MHC-linked HSP70 genes."; Immunogenetics 32:242-251(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rowen L., Madan A., Qin S., Shaffer T., James R., Ratcliffe A., Abbasi N., Dickhoff R., Loretz C., Madan A., Dors M., Young J., Lasky S., Hood L.;
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                                                                                                                                                                                                                                          shock; Multigene family.; 6D548263E98780F9 CRC64;
                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                                                                                                                                                                                                                                                        Score 42; DB :
Pred. No. 1.4;
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0; Mismatches
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                                                                                    PRINTS; PR00301; HEATSHOCK70.
Probom; PD000089; Hep70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS00329; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat sk
                                                                                                                                                                                                                                                                              70250 MW;
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88.9%;
HSSP; P08107; 1HJO.
InterPro; IPR001023; Hsp70.
Pfam; PF00012; HSP70; 1.
                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 86.>
---- 8; Conservative
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I -> V (IN REF. 2).
E -> D (IN REF. 3; AAD21816).
A -> G (IN REF. 2).
M SING (IN REF. 2).
N -> S (IN REF. 3; AAD21815).
                                                                    MIM; 603012; -.

R GO; GO:0005634; C:roytoplasm; TAS.

R GO; GO:0005634; C:mucleus; TAS.

R GO; GO:0005634; F.heat shock protein activity; TAS.

R GO; GO:0006402; P:mRNA catabolism; TAS.

R THERYPO; IPRO0123; HSp70.

R PRIMTS; PRO0301; HEANSHOCK70.

R PRODOM; PD000089; Hsp70; 1.

R PROSITE; PS00293; Hsp70; 1.

R PROSITE; PS00293; Hsp70; 2.

R PROSITE; PS01036; HSP70; 3; 1.

R PROSITE; PS01036; HSP70; 3; 1.

R PROSITE; PS01036; HSP70; 3; 1.
              SWISS-2DPAGE; P08107; HUMAN.
                             Genew; HGNC:5232; HSPAlA.
Genew; HGNC:5233; HSPAlB.
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CONFLICT
CONFLICT 31
CONFLICT 37
CONFLICT 46
CONFLICT 45
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WELLINE-99234376; PubMed=10216320;
WEDLINE-99234376; PubMed=10216320;
WEDLINE-99234376; PubMed=10216320;
WELLINE-99234376; PubMed=10216320;
WELLINE OF WALSH M.A., Freeman B.C., Morimoto R.I., Joachimiak A.;
Terructure of a new crystal form of human hsp70 ATPase domain.";
Acta Crystallogr. D 55:1105-1107(1999).
CHONTION: IN COOPERATION WITH OTHER CHAPERONES, HSP70S STABILIZE PREBXISTENT PROTEINS AGAINST AGGREGATION AND MEDIATE THE FOLDING OF NEWLY TRANSLATED POLYPEPTIDES IN THE CYTOSOL AS WELL AS WITHIN CHAPLES. THE HSP70S IN MITCHONDRIA AND THE ENDOPLASMIC OF PROTEIN TRANSLATION WITH HSP90. THEY PARTICIPATE IN ALL THESE CONFORMATIONS OF OTHER PROJUCTION IN SIGNAL TRANSLOCTION PROCESSES THROUGH THEIR ABILLITY OF RECONIZE NONNATIVE CONFORMATIONS OF OTHER PROFILES. THEY SHOULD PEPTIDE SURFACE SHORMS OF OTHER PROFILES. THEY SHOULD PEPTIDE SURFACE SHORMS OF OTHER PROFILES. THEY SHOULD PEPTIDE STREAMS-INDUCED DAMAGE.
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Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."; Proc. Natl. Acad. Sci. U.S.A., 99:16899-16903 (2002).
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MEDLINE=87066768; PubMed=3786141;
Drabent B., Genthe A., Benecke B.-J.;
"In vitro transcription of a human hsp 70 heat shock gene by extracts prepared from heat-shocked and non-heat-shocked human cells.";
Nucleic Acids Res. 14:8933-8949(1986).
                                                                                                                                                                                SEQUENCE OF 1-36 AND 360-424 FROM N.A.
MEDLINE=89184548; PubMed=2538825;
Sargent C.A., Dunham I., Trowsdale J., Campbell R.D.;
"Human major histocompatibility complex contains genes for the major heat shock protein HSP70.";
Proc. Natl. Acad. Sci. U.S.A. 86:1968-1972(1989).
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BC002453; AAH02453.1;
BC003322; AAH0922.1;
BC018740; AAH18440.1;
M24743; AAA59844.1;
M2474; AAA59845.1;
XO44677; CAA28381.1;
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AF134726; AAD21815.1;
AP000503; BAB63300.1;
AP000503; BAB63299.1;
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EMBL; M59830; AAA63227.1; -.
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A29160; A29160. A45871; A45871. I59139; I59139. I79540; I79540. 1HJO; 21-0CT-98

PIR; PIR; PIR; PIR; PDB;

EMBL; EMBL; EMBL; EMBL; EMBL; EMBL;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete nucleotide sequence of a porcine HSP70 gene.";
Immunogenetics 35:286-289(1992).
-!- FUNCTION: In cooperation with other chaperones, Hsp70s stabilize
                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDILIBE-92175874; PubMed=1339404; MEDILIBE-92175874; PubMed=1339404; Pee-lman L.J., de Weghe A.R., Coppieters W.R., van Zeveren A.J., Bouquet Y.H.;
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                                                                             Length 641;
                                                                                                             1; Indels
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                                                                              Score 42; DB 1;
Pred. No. 1.4;
                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Heat shock 70 kDa protein 1 (HSP70.1).
                                                                                                               0; Mismatches
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PIR; S35718; S35718.
HSSP; P08107; 1HJO.
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PRINTS; PR00301; HEATSHOCK70.
PRODOM; PD000089; HSP70; 1.
PROSITE; PS00229; HSP70_1; 1.
PROSITE; PS01036; HSP70_2; 1.
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                                                                             91.3%;
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                                                                                              Local Similarity 88.9
nes 8; Conservative
                                                                                                                                                                                                                                                               STANDARD;
               342
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nes 8; Conserv
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HS71_PIG
ID HS71 PIG
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Biochim. Biophys. Acta 1219:64-72(1994).
Biochim. Biophys. Acta 1219:64-72(1994).
Prox. Biochim. Biophys. Acta 1219:64-72(1994).

preex. Steen proteins against aggregation and mediate the folding of newly translated polypeptides in the cytosol as well as within organelles. These chaperones participate in all these processes through their ability to recognize nomative conformations of other proteins. They bind extended peptide segments with a net hydrophobic character exposed by polypeptides during translation and membranslocation, or following stress-induced damage.

-!- INDUCTION: By heat shock.
-!- SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=LBW 1W/GIN;
MEDLINE=95012453; PubMed=7927536;
Walter L., Rauh F., Guenther E.;
"Comparative analysis of the three major histocompatibility complex-linked heat shock protein 70 (Hsp70) genes of the rat.";
Immunogenetics 40:325-330(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Longo F.M., Wang S., Narasimhan P., Zhang J.S., Chen J., Massa S.M., Sharp F.R., "cDNa cloning and expression of stress-inducible rat hsp70 in normal and injured rat brain.";
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MEDLINE-94368874; PubMed-8086479;
Lisowska K., Krawczyk Z., Widlak W., Wolniczek P., Wisniewski J.;
"Cloning, nucleotide sequence and expression of rat heat inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00297; HSP70; 1.
PROSITE; PS00297; HSP70_1; 1.
PROSITE; PS01036; HSP70_2; 1.
PROSITE; PS01036; HSP70_3; 1.
ATP-binding; Chaperone; Heat shock; Multigene family.
CONFLICT 71 72; KR -> NG (IN REF. 3).
                                       007439; P42853;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
HSP70-1 AND HSP70-2.
641 AA
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EMBL; X77208; CAA54423.1; ---
EMBL; X74201; CAA54422.1; ---
EMBL; X74271; CAA542228.1; ---
PIR; I54542; I54542.
InterPro; IPR001023; HSp70.
Pfam; PP00012; HSp70; IPR001024; HSp70.
PFINTY; PR00301; HSP70; IPR001025; HSP70.
PRINTY; PR00301; HSP70; IPR00103; HSP70; IPR00103; HSP70; IPR00103; HSP70; IPR00103; HSP70; IPR00103; HSP70; IPR00103; HSP70; IPR010103; HSP70; IPR010103; HSP70; IPR010103; HSP70; IPR010103; HSP70; IPR010103; HSP70; IPR010103; IPR01
    STANDARD;
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FEWS Microbiol. Lett. 137:1-8(1996).
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MEDLINE=S95028152; PubMed=7941740;
MEDLINE=95028152; PubMed=7941740;
Clark M.W., Keng T., Storms R.K., Zhong W., Fortin N., Zeng B.,
Delaney S., Ouellette B.F.E., Barton A.B., Kaback D.B., Bussey H.;
"Sequencing of chromosome I of Saccharomyces cerevisiae: analysis of
Yeast 10:535-541(1994).
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"The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.";
Nucleic Acids Res. 17:805-806(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S., "Protein identifications for a Saccharomyces cerevisiae protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota, Fungi, Ascomycota, Saccharomycotina, Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 590-641 FROM N.A.
MEDLINE-85087943; PubMed-6096826;
Ogden R.C., Lee M.-C., Knapp G.;
"Transfer RNA splicing in Saccharomyces cerevisiae: defining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACETYLATION.
Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B.
                                                                                                                                 0;
                                                                                      Score 42; DB 1; Length 641; Pred. No. 1.4;
                                                                                                                               Indels
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    D -> H (IN REF. 2 AND 3).
G -> A (IN REF. 3).
D02D96751C868583 CRC64;
                                                                                                                                                                                                                                                                                                                                                    01-JUL-1989 (Rel. 11, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Heat shock protein SSA1 (Heat shock protein YG100).
SSA1 OR YALOSC.
                                                                                                                                                                                                                                                                                                                      641 AA.
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                                                                                                                                                                                                                                                                                                                 PRT;
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MEDLINE=89128457; PubMed=2644626;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=95203288; PubMed=7895733;
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MEDLINE=97089742; PubMed=8935650;
                                             70163 MW;
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                                                                                      91.3%;
                                                            Query Match
Best Local Similarity 88.3°,
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                                                                                                                                                                   SLFEGIDIY 9
    227 2
408 4
641 AA;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the EMSL outstation. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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GO; GO:0000277; C:cell wall (sensu Fungi); IDA.

GO; GO:0005737; C:cell wall (sensu Fungi); IDA.

GO; GO:0005737; C:cell wall

GO; GO:0005824; C:undleus; IDA.

GO; GO:00016887; F:ATPass activity; IDA.

GO; GO:0006457; F:ATPass activity; IDA.

GO; GO:00006457; P:protein folding; IDA.

GO; GO:0000665; P:protein-nucleus import, translocation; IDA.

GO; GO:000066; P:protein-nucleus import, translocation; IDA.

GO; GO:0000606; P:Protein-nucleus cotranslational membrane targ. . .; IDA.
SUDMITTED (SEP-1994) tO SWISS-PrOT.

-1- FUNCTION: SSA1 MAY PLAY A ROLE IN THE TRANSPORT OF POLYPEPTIDES BOTH ACROSS THE MITOCHONDRIAL MEMBRANES AND INTO THE ENDOPLASMATIC RETICULUM. A FUNCTIONAL DIFFERENCE BETWEEN YEAST SSA1 AND SSA2 PROTEINS IS EXPECTED. SSA1 CAN PARTICIPATE IN THE ATP-DEPENDENT DISASSEMBLY OF CLATHRIN-COATED VESICLES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                          SUBCELLULAR LOCATION: Cytoplasmic. SIMILARITY: Belongs to the heat shock protein 70 family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 641;
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PROSITE; PS00297; HSP70 1; 1.

PROSITE; PS01036; HSP70 2; 1.

PROSITE; PS01036; HSP70 3; 1.

Heat shock; ATP-binding; Multigene family; Acetylation.

MOD_RES. 1

ACETYLATION.
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FA9389BAE9B1D7DA CRC64;
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88.9%; Pred. No. 1.4;
iive 0; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X12926; CAA31393.1; -.
EMBL; L22015; AAC04952.1; ALT_SEQ.
PIR; S43449; HHBYA1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HSSP, P19120; 3HSC. -
GermOnline, 138348; -
NMISS-2DPAGE; P10591; YEAST.
COMPLUYEAST-2DPAGE; P10591; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   641 AA; 69526 MW;
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PRINTS; PR00301; HEATSHOCK70.
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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                  Copyright
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- protein search, using sw model OM protein

Run on:

September 15, 2004, 10:31:26; Search time 11.3684 Seconds (without alignments) 76.152 Million cell updates/sec

US-09-673-795-1 46 SLFEGIDIY 9 score: Sequence: Perfect

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

283366

seq length: 0 seq length: 200000000 DB DB Minimum | Maximum |

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	TOTOGER	aK-tvpe	dnaK-tvpe molecula		- 4				probable heat shoc	400											Tub-Low Lub-Low				Fundlow	100000	molecul fundam	Type molecul	molecul function	protei
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dnaK-type molecula dnaK-type molecula	heat shock protein heat shock protein	dnak-type molecula	dnaK-type molecula	dnaK-tvpe molecula	heat-shock protein	heat-shock protein	dnaK-type molecula	heat shock protein	dnaK-type molecula	dnaK-tvpe molecula	heat shock protein	heat shock protein
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330	3 6	3 4 3 5	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

dnak-type molecular chaperone HSC70 - California sea hare (fragment)

NyAlternate names: heat shock protein 70 homolog HSC70

SySpecies: Aplyaia californica (California sea hare)

CyBedeis: B4261

Ayritle: Long-term sensitization training in Aplysia leads to an increase in the expres Ayrecession: B44261

Ayrection: Ayrection training in Aplysia leads to an increase in the expres Ayrecession: B44261

Ayrection: Decliminary not compared with conceptual translation

Ayrection: preliminary not compared with conceptual translation

Ayrection: Sequence extracted from NCBI backbone (NCBIP:118950)

A;Gene: HSC70 C;Function:

A,Description: involved in protein folding and assembling/disassembling of protein comp. C,Superfamily: heat shock protein 70 C,Keywords: ATP; molecular chaperone

. 0 Length 208; 1; Indels DB 2; Pred. No. 0.52; 0; Mismatches Score 42; Pred. No. 91.3%; 8; Conservative Query Match Best Local Similarity Best Loc Matches

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Gaps

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dnaK-type molecular chaperone (clone pTHS70.7) - rainbow trout (fragment) N;Alternate names: 70K heat shock protein C;Species: Oncorhynchus mykiss (rainbow trout) C;Pate: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 20-Aug-1999

CjAccession: IS1344
R;Kothary, R.K.; Jones, D.; Candido, E.D.M.
Mol. Cell. Biol. 4, 1785-1791, 1984
A;Title: 70-kilodalton heat shock polypeptides from rainbow trout: Characterization of cA;Reference number: IS1344; MUID:85036330; PMID:6092938

A,Accession: 151344 A,Status: preliminary; translated from GB/EMBL/DDBJ A,Molecule type: mRNA

A; Residues: 1-278 < KOT>

A;Description: involved in protein folding and assembling/disassembling of protein compl C;Superfamily: heat shock protein 70 C;Keywords: ATP; molecular chaperone A;Cross_references: GB:K02549; NID:g213803; PIDN:AAA49562.1; PID:g213804 C;Function:

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(Species: Eunicella cavolini
(Species: Bunicella cavolini
(Spate: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
(Accession: T45478
Riborchiellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A.Reference number: Z22983
A.Accession: T45478
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Pred. No. 1.3;
0; Mismatches 1; Indels
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R;Borchiellini, C.; Le Parco, Y.
submitted to the EMBL Data Library, September 1997
A;Reference number: Z22983
A;Accession: T45479
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-467 -460R>
A;Cross-references: EMBL:AF026520; PIDN:AAC05364.1
C;Genetics:
A;Genetics:
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88.9%; Pred. No. 1.3;
tive 0; Mismatches 1
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C;Genetics:
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88.9%; Pred. No.
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Best Local Similarity 88.9%;
Matches 8; Conservative (
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Best Local 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                253 SLFEGIDFY 261
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Best Local Similarity
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J. Biol. Chem. 261, 2102-2112, 1986
A; Title: Molecular cloning and analysis of DNA complementary to three mouse Mr=68,000 he
A; Reference number: A26283; MUID:86111900; PMID:2868009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A. Accession: A26283
A. Molecule type: mRNA
A. Molecule type: mRNA
A. Kesidues: 1-420 < LONA
A. Cross-references: GB: M12571; NID: 9194014; PIDN: AAA57234.1; PID: 9387208
A. Note: the authors translated the codon CTG for residue 173 as Val and CGC for residue C. Function:
C. Function:
A. A. Description: involved in protein folding and assembling/disassembling of protein compl. C. Superfamily: heat shock protein 70
C. Superfamily: heat shock protein 70
C. Keywords: ATP; molecular chaperone
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C;Species: Chondrosia reniformis
C;Dacies: Chondrosia reniformis
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45477
R;Borchiellini, C:; Le Parco, Y.
submitted to the BMBL Data Library, September 1997
A;Reference number: 222983
A;Reference number: 222983
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C;Species: Bunicella cavolini
C;Date: 31-Jan-2000 #sequence_revision 31-Jan-2000 #text_change 21-Jul-2000
C;Accession: T45479
                                                                                                                                                                                                                                                                                                                                                                                         dnaK-type molecular chaperone - mouse (fragment)
NiAlterrate names: heat shock protein 68
C.Specias: Mus musculus (house mouse)
C.Specias: Mus musculus (house mouse)
C.Specia: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Aug-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.3%; Score 42; DB 2; Length 420; 88.9%; Pred. No. 1.1;
                                         Score 42; DB 2; Length 278;
Pred. No. 0.72;
0; Mismatches 1; Indels
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A, Molecule type: mRNA
A, Residues: 1-467 < 405A
A, Cross-references: EMBL. AP026517; PIDN:AAC05362.1
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                                                   91.3%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88...
8; Conservative
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Matches 8; Conservative
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T45479
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A;Residues: 1-636 <EDD>
A;Cross-references: GB:L22736; NID:g433179; PIDN:AAA33219.1; PID:g433180
A;Note: authors translated the codon ACA for residue 10 as Pro, GCT for residue 60 as V;
                                                                                                                                                                                                                                                                                                                             C)Function:
A;Description: involved in protein folding and assembling/disassembling of protein comp
C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R,Eddy, R.J.; Sauterer, R.A.; Condeelis, J.S.
J. Biol. Chem. 268, 23267-23274, 1993
A;Title: Aginactin, an agonist-regulated F-actin capping activity is associated with an
A;Reference number: A48872; MUID:94043116; PMID:8226849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dnak-type molecular chaperone hspB - slime mold (Dictyostelium discoideum) (fragment) N/Alternate names: 70k heat shock cognate protein aginactin; F-actin capping protein ag
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NyAlternate names: heat shock protein 70
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Species: Cercopithecus aethiops (green monkey, grivet)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Aug-1999
C;Accession: S31766, 136927
E;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
Submitted to the EMBL Data Library, January 1993
A;Description: Nucleotide sequence of the CDNA encoding a monkey 70kd heat shock protein
A;Reference number: S31766
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A;Molecule type: mRNA
A;Molecule type: mRNA
A;Kesidues: 1-638 <5AI>
B;Sainis, I.; Angelidis, C.; Pagoulatos, G.; Lazaridis, I.
FEBS Lett. 355, 282-286, 1994
A;Title: The hsc70 gene which is slightly induced by heat is the main virus inducible
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C;Date: 19-May-1995 #sequence_revision 19-May-1995 #text_change 20-Aug-1999
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88.9%; Pred. No. 1.8;
iive 0; Mismatches 1
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Pred. No. 1.8;
0; Mismatches
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Matches 8; Conserv
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                                                                                             probable heat shock protein [imported] - Arabidopsis thaliana C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: Arabidopsis thaliana (mouse-ear cress)
C.Species: A.; Bcker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; K.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, A.Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A.H. Herence number: A86141; MulD:21016719; PMID:11130712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    daak-type molecular chaperone hsc70 [imported] - slime mold (Dictyostelium discoideum)
N;Alternate names: heat shock cognate protein 70
G;Species: Dictyostelium discoideum
C;Species: Dictyostelium discoideum
C;Accession: T45471
R;Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.
R;Boves, H.; Mintert, U.; Dittrich, W.; Faix, J.; Gerisch, G.
A;Reference number: Z22980
A;Accession: T45471
A;Status: preliminary; translated from GB/EMBL/DDBJ
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2; Length 617;

Score 42; DB 2; Pred. No. 1.7; 0; Mismatches

91.3%;

Query Match Best Local Similarity 88.2 Best Local Similarity 88.2

292 SLFEGIDFY 300

1 SLFEGIDIY 9

8 임

A;Map position: 1 C;Superfamily: heat shock protein 70

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-617 <STO>

me

Length 632; Indels

Score 42; DB 2; Pred. No. 1.8;

91.3%;

Query Match Best Local Similarity 88.50, -169 8; Conservative

SLFEGIDFY 293

g à

SLFEGIDIY 9

A;Cross-references: EMBL:AF025951; PIDN:AAB81865.1 A;Experimental source: strain AX3

C;Genetics:

A; Residues: 1-632 <BOV>

A;Gene: hsc70 A;Note: localized to filopodias and cortex C;Superfamily: heat shock protein 70

1;

0; Mismatches

dnak-type molecular chaperone - chicken N;Alternate names: heat shock protein 70 C;Species: Gallus gallus (chicken)

RESULT 10 A25646

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A; Accession: S64772
A; Molecule type: DWA
A; Residues: 1-639 < GGF>
A; Cross_references: EMBL: Z73129; NID: g1360201; PIDN: CRA97472.1; PID: g1360202; MIPS: YLLO
A; Experimental source: strain S288C
A; Experimental source: strain S288C
Submitted to the Protein Sequence Database, May 1996
A; Reference number: S64775
A; Accession: S64775
A; Accession: S64775
A; Accession: S64775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A) Experimental source: strain 5288C
R; Purnelle, B.; Goffeau, A.
submitted to the EMBL Data Library, April 1996
A; Pescription: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14
A; Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals 14
A; Reference number: $69380
A; Recession: $69383
A; Residues: 1-639 < PUR>
A; Residues: 1-639 < PUR>
A; Construction: Full Pure Number: $60380
A; Construction: $60380
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C;Superfamily: heat shock protein 70
C;Keywords: ATP; molecular chaperone
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R;Smutch, T.P.; Heschl, M.F.P.; Baillie, D.L.
Gene 4, 241-255, 1988
A;Title: The Caenchabditis elegans hsp70 gene family: a molecular genetic characteriz
A;Reference number: JT0285; MUID:88297155; PMID:2841196
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: involved in protein folding and assembling/disassembling of protein com C; Superfamily: heat shock protein 70 C; Keywords: ATP; heat shock; molecular chaperone; stress-induced protein
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N/Alternate names: heat shock protein 70 A
Cispecies: Caenorhabditis elegans
Cispecies: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 22-Jun-1999
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Pred. No. 1.8;
0; Mismatches
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Pred. No. 1.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: MIPS: YLL024c; SGD: S0003947
                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: DNA
A;Residues: 72-639 <DUE>
A;Cross-references: EMBL:Z73129; MIPS:YLL024c
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88.9%;
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A; Introns: 69/1; 331/3; 558/3
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A; Residues: 1-640 <SNU>
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Best Local Similarity
...as 8; Conserve
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Best Local Similarity
Matches 8; Conserv
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                                                                                   A)Attatus: preliminary; translated from GB/EMBL/DDBJ
A)Altatus: preliminary; translated from GB/EMBL/DDBJ
A)Attatus: preliminary; translated from GB/EMBL/DDBJ
A)Attatus: 1-638 aRES
A)Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A)Cross-references: EMBL:X70684; NID:g22781; PIDN:CAA50019.1; PID:g22782
A)Genetics:
A)Genetics:
A)Genetics:
A)Genetics:
A)Abescription: involved in protein folding and assembling/disassembling of protein compl
C;Buperfamily: heat shock protein 70
C;Buperfamily: heat shock protein 70
C;Buperfamily: heat shock protein 70
C;Buperfamily: heat shock protein 70
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Gene 121, 353-358, 1992
A,Title: Characterization of a new member of the sea urchin Paracentrotus lividus hsp70
A,Reference number: JC1391; MUID:93077053; PMID:1339375
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N;Alternate names: heat shock protein YG102; protein L0971; protein XLL024c
C;Species: Saccharomyces cerevisiae
C;Date: 07-May-1993 #sequence revision 07-May-1993 #text_change 20-Jun-2000
C;Accession: S20139; S64772; S64775; S69383
R;Slater, M.R.; Craig, E.A.
Nucleic Acids Res. 17, 805-806, 1989
A;Title: The SSA1 and SSA2 genes of the yeast Saccharomyces cerevisiae.
A;Reference number: S20139; MUID:89128457; PMID:2644626
A;Accession: S20139
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-639 cSLA3
A;Residues: 1-639 cSLA3
A;Residues: 1-639 cSLA3
A;Residues: 1-639 cSLA3
A;Goffeau, A.; Purnelle, B.
Submitted to the Protein Sequence Database, May 1996
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C;Species: Paracentrotus lividus (common urchin)
C;Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 20-Aug-1999
C;Accession: JC1391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A,Cross-references: EMBL:X61379; NID:g312916; PIDN:CAA43653.1; PID:g312917 C,Genetics:
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N,Alternate names: heat shock protein 70IV; hsp70IV protein
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Larity 88.9%; Pred. No. 1.8;
Conservative 0; Mismatches 1; Indels
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                              A;Reference number: 136927; MUID:95080396; PMID:7988690 A;Accession: 136927
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Pred. No. 1.8;
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A; Residues: 1-639 <SCO>
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Best Local Similarity
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287 SLFEGIDFY 295

Search completed: September 15, 2004, 10:36:13 Job time : 11.3684 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

September 15, 2004, 10:34:32; Search time 40.7368 Seconds (without alignments) 29.609 Million cell updates/sec Run on:

US-09-673-795-1 46 1 SLFEGIDIY 9 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

725134 Total number of hits satisfying chosen parameters:

725134 seqs, 134019282 residues

Searched:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Pending Patents AA New:*

1: /cgn2 6/ptodata/2/paa/PCT NEW COMB.pep:*

2: /cgn2 6/ptodata/2/paa/US06_NEW COMB.pep:*

3: /cgn2 6/ptodata/2/paa/US08_NEW-COMB.pep:*

5: /cgn2 6/ptodata/2/paa/US08_NEW-COMB.pep:*

6: /cgn2 6/ptodata/2/paa/US09_NEW-COMB.pep:*

6: /cgn2 6/ptodata/2/paa/US09_NEW-COMB.pep:*

7: /cgn2 6/ptodata/2/paa/US09_NEW-COMB.pep:*

7: /cgn2 6/ptodata/2/paa/US00_NEW-COMB.pep:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Reminence 20060	000	educarce	equence 129	equence 14304,	equence 8613.	8613	egnende	emience 47005	odience 861	oducento o	1 6	i c	educance 320	eduence 740	ednence 121	equence 22,	326	equence 6, A	621	623	equence 625	SCS SOURIES	9 0	'ac aoman's	53	54	Sequence 55, Appl
σι	US-10-767-701-33352	-10-885-523-12	-60-565-632-1	-60-579-062-1295	-10-425-115-34	-565-632-8613	US-60-579-062-8613	-581-351-2	01-470	-565-632-8611	-60-579-062-861	-60-581-351-201	-10-501-035-326	09-949-0030-2	0 1 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	10 010 011	-10-3/0-/15B-22	170-205	10-926-802-6	-69-	-60-566-425-6	566-42	US-60-566-425-626	-60-570-505-52	#60-E70-E0E	-60-3/0-303-3	0-00-00-00-	US-60-570-505-55
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Sequence 497, Apple Sequence 27, Apple Sequence 28, Apple Sequence 29, Apple Sequence 63, Apple Sequence 653, Apple Sequence 655, Apple Sequence 658, Apple Sequence 658, Apple Sequence 41, Apple Sequence 42, Apple Sequence 44, Apple Sequence 44, Apple Sequence 44, Apple Sequence 44, Apple Sequence 44, Apple Sequence 44, Apple Sequence 146, Appl	Sequence 2015, Appliated Sequence 2017, Appliated Sequence 2017, Appliated 2019, Appliated 201
1 7 US-60-570-505-497 1 7 US-60-576-801-28 1 7 US-60-576-801-28 1 7 US-60-576-801-28 1 7 US-60-576-801-403 1 7 US-60-576-812-653 1 7 US-60-576-812-657 1 7 US-60-576-812-657 1 7 US-60-592-191-41 1 7 US-60-592-191-42 1 7 US-60-592-191-44 1 7 US-60-592-191-44	77
91.3 641.3 6	
272 208 3 3 3 3 3 2 2 8 8 2 2 8 8 3 3 3 3 3 3	43 44 45 45 42

ALIGNMENTS

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APPLICANT: Evalic, David K.
APPLICANT: Evalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwa K.
APPLICANT: Cao, Yongwa K.
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
TITLE OF INVENTION: NUMBER: 2004.01.29
CURRENT APPLICATION NUMBER: 2004.01.29
SEQ ID NOS: 63128
LENGTH: 181
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US-10-767-701-33352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.3%; Score 42; DB 6;
88.9%; Pred. No. 1.3;
tive 0; Mismatches 1
                          ; Sequence 33352, Application US/10767701; GENERAL INFORMATION:
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Best Local Similarity 88.9
Matches 8, Conservative
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US-10-767-701-33352
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Sequence 12, Application US/10885523

| GENURAL INFORMATION: | APPLICANT: Huang, Qian | APPLICANT: Huang, Qian | APPLICANT: Huang, Qian | F.L. | APPLICANT: Cho, Bryan K. | APPLICANT: Cho, Bryan K. | APPLICANT: Palliser, Deborah | APPLICANT: Chen, Jianzhu | APPLICANT: Chen, Jianzhu | APPLICANT: Chen, Jianzhu | APPLICANT: Fisen, Herman N. | APPLICANT: Young Richard A. | TITLE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is TITLE OF INVENTION: CD4+T Cell-Independent | TITLE OF INVENTION: CD4+T Cell-Independent | TITLE OF INVENTION NUMBER: US/10/885,523 | CURRENT APPLICATION NUMBER: US/10/805,523 | CURRENT APPLICATION NUMBER: US/09/761,534 | PRIOR FILING DATE: 2001-01-16 RESULT 2 US-10-885-523-12

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US-10-425-115-345997

US-10-425-115-345997, Application US/10425115

Sequence 345997, Application US/10425115

GENERAL INFORMATION:

APPLICANT: La Rosa, Thomas J.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants

TITLE OF INVENTION: Plants

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 345997

LENGTH: 296
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APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Larosa, Thomas J.
APPLICANT: Lu, Maolorg
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: APPLICANT: Zhang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants an
TITLE OF INVENTION: Compositions Thereof
FILE REFERENCE: 38-21(53403)B
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT FILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 15449
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LOCATION: (1)..(296)
OCHER INFORMATION: unsure at all Xaa locations
FEATURE:
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Pred. No. 2.3;
0; Mismatches
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CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: PatentIn version 3.2
SEQ ID NO 12954
LENGTH: 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8613, Application US/60565632
GENERAL INFORMATION:
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                                                                                                                                                ; ORGANISM: Diabrotica virgifera
US-60-579-062-12954
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Best Local Similarity 88.5
Local 8, Conservative
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Best Local Similarity 88.5
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APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Baum, James A
APPLICANT: Larosa, Thomas J
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maolong
APPLICANT: Munylkva, Tichifa R. I.
APPLICANT: Wu, wei
APPLICANT: Wu, wei
APPLICANT: Wu, wei
APPLICANT: Mu, wei
APPLICANT: Alang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions thereof
FILE REPERENCE: 38-21 (53403) C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MULYLWA, Tichifa R. I.
APPLICANT: MULYLWA, Tichifa R. I.
APPLICANT: MULYLWA, Tichifa R. I.
APPLICANT: Mulylwa, Tichifa R. I.
APPLICANT: Muly Wei
APPLICANT: Charge Bei
TITLE OF INVENTION: Compositions Thereof
TITLE OF INVENTION: Compositions Thereof
TITLE REPERENCE: 38-21 (53403) B
CURRENT APPLICATION NUMBER: US/60/565,632
CURRENT PILING DATE: 2004-04-27
NUMBER OF SEQ ID NOS: 154499
SOFTWARE: Patentin version 3.2
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Pred. No. 1.5;
                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                          FEATURE:
, OTHER INFORMATION: Murine hsp70 - Segment II US-10-885-523-12
                                                                                                                                                                                                                                                                                                                                                0; Mismatches
          PRIOR APPLICATION NUMBER: PCT/US00/32831
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-12-01
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PASLERQ for Windows Version 4.0
SEQ ID NO 12
LENGTH: 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-60-565-632-12954
; Sequence 12954, Application US/60565632
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Baum, James A
Kovalic, David K.
Larosa, Thomas J.
Lu, Maolong
Munyikwa, Tichifa R. I.
Roberts, James K.
Wu, Wei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Monsanto Technology, LLC APPLICANT: Baum, James A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) ORGANISM: Diabrotica virgifera
US-60-565-632-12954
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88.9%;
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Best Local Similarity 88.9%;
Matches 8; Conservative (
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Best Local Similarity 88.9
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97 SLFEGIDFY 105
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                                                                                                                                                                                                       ORGANISM: Unknown
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US-60-579-062-12954
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LENGTH: 263
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APPLICANT:
APPLICANT:
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us-09-673-795-1.rapn

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...use5632
...useB1CANT: Baum, James A
...use65632
...useB1CANT: Baum, James A
...appLICANT: Baum, James A
...appLICANT: Larosa, Thomas J.
...appLICANT: Larosa, Thomas J.
...appLICANT: Munyikwa, Trinifa R. I.
...appLICANT: Roberts, James K.
...appLICANT: Roberts, James K.
...appLICANT: Roberts, James K.
...appLICANT: Compositions Thereof
...appLICANT: Compositions Thereof
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...appLICANT: AppLICATION NUMBER: US/60/565,632
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                                                                                                                                                                                                                           Sequence 47005, Application US/10767701

GENERAL INFORMATION:

APPLICANT: Kovalic, David K.

APPLICANT: Zhou, Yihua

APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement

TITLE OF INVENTION: Plants us/10/767,701

CURRENT APPLICATION NUMBER: US/10/767,701

CURRENT PILING DATE: 2004-01-29

NUMBER OF SEQ ID NOS: 63128

LENGTH: 601
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; LOCATION: (69)...(69)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-565-632-8611
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US-10-767-701-47005
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Pred. No. 4.8;
0; Mismatches
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OTHER INFORMATION: unsure at all Xaa locations
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88.9%;
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ORGANISM: Diabrotica virgifera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Sorghum bicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 88.9
Matches 8; Conservative
                                                                                         154 SLFEGIDFY 162
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OTHER INFORMATION: Xaa
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NAME/KEY: unsure
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APPLICANT: Zhang, Bei

TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions thereof

TITLE REFERENCE: 38-21 (53403) C
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 41445
SOFTWARE: Patentin version 3.2
TENCOME. 10 8613
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
TITLE OF INVENTION: UNGBER: US/60/581,351
CURRENT APPLICATION WUMBER: US/60/581,351
CURRENT FILING DATE: 2003-66-19
PRIOR FILING DATE: 2003-66-19
NUMBER OF SEQ ID NOS: 13860
SOFTWARE: Patentin version 3.2
ISROIN 00.205
TYPE: PRI
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Pred. No. 4;
0; Mismatches 1; Indels
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Pred. No. 2.9;
0; Mismatches
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APPLICANT: Baum, James A
APPLICANT: Kovalic, David K
APPLICANT: Larcsa, Thomas J
APPLICANT: Lu, Maclong;
APPLICANT: Lu, Maclong;
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
                                                                                                                                         ) ORGANISM: Diabrotica virgifera
US-60-565-632-8613
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SOFTWARE: Patentin version 3.2
SEQ ID NO 8613
LENGTH: 376
TYPE: PRT
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US-60-581-351-2025
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PAPELICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTING
TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KINAS
TITLE OF INVENTION: AND/OR PROTEIN TYROSINE KINASE PATHWAYS
FILE REFRERENCE: DO1895 PCT
CURRENT APPLICATION NUMBER: US/10/501,035
CURRENT PILING DATE: 2004-07-09
PRIOR FILING DATE: 2004-07-09
NUMBER OF SEQ ID NOS: 795
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
LENGTH: 640
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TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: DISORDERS, METHODS OF DETECTION AND USES THEREOF
TILE REPERENCE: CLOO0791
CURRENT APPLICATION NUMBER: US/09/949,003C
CURRENT FILING DATE: 2001-09-10
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 74065
SOFTWARE: Patentin version 3.2
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GENERAL INFORMATION:
APPLICANT: Labar, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
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ORGANISM: Homo sapiens
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US-10-821-234-1519
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APPLICANT: Larosa, Thomas J
APPLICANT: Larosa, Thomas J
APPLICANT: La, Maclong
APPLICANT: Lu, Maclong
APPLICANT: Roberts, James K
APPLICANT: Roberts, James K
APPLICANT: Roberts, James K
APPLICANT: Roberts, James K
APPLICANT: Roberts, James K
APPLICANT: Shang, Bei
TITLE OF INVENTION: Methods for Genetic Control of Insect Infestations in Plants and
TITLE OF INVENTION: Compositions thereof
FILE REFERENCE: 38-21 (53403) C
CURRENT APPLICATION NUMBER: US/60/579,062
CURRENT FILING DATE: 2004-06-11
NUMBER OF SEQ ID NOS: 414455
SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: Nucleic Acid Molecules Associated With Protein In Plants
FILE REFERENCE: 38-21(53372)B
CURRENT APPLICATION NUMBER: US/60/581,351
CURRENT FILING DATE: 2004-06-17
PRIOR FILING DATE: 2003-06-19
NUMBER OF SEQ ID NOS: 13980
SOFTWARE: Patentin version 3.2
SOFTWARE: Patentin version 3.2
SEQ ID NO 2016
LENGTH: 639
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; LOCATION: (69)...(69)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-60-579-062-8611
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OTHER INFORMATION: Xaa can be any naturally occurring amino acid
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91.3%; Score 42; DB 7; Length 639; 88.9%; Pred. No. 5.2; ive 0; Mismatches 1; Indels
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Pred. No. 5.2;
0; Mismatches
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APPLICANT: Kovalic, David K
APPLICANT: Larosa, Thomas J
APPLICANT: Lu, Maclong
APPLICANT: Munyikwa, Tichifa R. I.
APPLICANT: Roberts, James K
APPLICANT: Wu, Wei
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US-60-579-062-8611
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LENGTH: 639
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### TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia CURRENT APPLICATION NUMBER: US/10/821,234

#### CURRENT APPLICATION NUMBER: US/04/62,047

#### PRIOR APPLICATION NUMBER: US 60/462,047

#### PRIOR PILING DATE: 2003-04-07

### PRIOR PILING DATE: 2003-04-07

### PRIOR PILING DATE: 2003-04-07

### NUMBER OF SEQ ID NOS: 1704

### SOFTWARE: PE SEQ genes Version 1.0

### INVER: PRT

### ORGANISM: Homo sapiens

US-10-821-234-1519

Query Match

### Score 42; DB 6; Length 641;

### Best Local Similarity 88.9%; Pred. No. 5.2;

### Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps

QV 1 SLFEGIDIY 9

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Sequence 117, Application PC/TUS0316736
SEPERAL INFORMATION:
APPLICANT: Wang, Rong-fu
TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
FILE REFERENCE: HO-P02484W00
CURRENT APPLICATION NUMBER: PCT/US03/16736
CURRENT FILING DATE: 2003-05-28
PRIOR PLING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 148
SOFTWARE: Patentin Version 3.1
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Pred. No. 5.5e+06;
            US-00-673-795-1

US-10-673-795-1

US-10-110-731-1

US-10-673-795-1

US-10-673-795-2

US-10-110-731-2

US-09-673-795-8

US-09-673-795-8

US-09-673-795-8

US-09-673-795-8

US-09-673-795-8

US-09-711-257-12033

US-09-711-577-12033

US-09-711-577-12033

US-09-711-577-12033

US-09-711-577-12033

US-09-791-577-12033

US-09-791-577-12033

US-10-328-953-319

US-10-328-953-319

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.08;
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Best Local Similarity
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                                                                                                                                                  September 15, 2004, 10:34:17; Search time 281.368 Seconds (without alignments) 31.221 Million cell updates/sec
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/ptodata/2/paa/US107_COMB.pep.
/ptodata/2/paa/US60_COMB.pep.*
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                                                                                                                                                                                                                                                                                                                                     6019581 seqs, 976053577 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                         protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length DB
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Score

Result No. 0

Gaps

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AFFILACANI: INTERDAN, CARDERINE
TITLE OF INVENTION: MUTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USEFUL IN CANCER
TITLE OF INVENTION: MUTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USEFUL IN CANCER
TITLE OF INVENTION: IMMUNOTHERAEY
FILE REFERENCE: 03715.0069
CURRENT APPLICATION NUMBER: US/09/673,795
CURRENT FILING DATE: 1999-04-22
PRIOR PILING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 8
SEQ ID NO S: 8
SEQ ID NO S: 2.1
SEQ ID NO S: 2.1
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TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis FILE REFERENCE: HO-P02484US1
CURRENT APPLICATION WUMBER: 12/10/447,161
CURRENT FILING DATE: 2003-05-28
PRIOR APPLICATION NUMBER: 60/383,530
PRIOR FILING DATE: 2002-05-28
NUMBER OF SEQ ID NOS: 148
SOFTWARE: Patentin version 3.1
SEQ ID NO 117
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Sequence 2, Application US/10110731

Sequence 2, Application US/10110731

Sequence 2, Application US/10110731

SEQUENCE 2.

THORMATION: NEW LYMPHOCYTES, A PROCESS FOF TITLE OF INVENTION: THERE USE IN THERAPEUTICS TITLE OF INVENTION: THERE USE IN THERAPEUTICS TITLE OF INVENTION: WORD 99 BA IDM STRE CURRENT APPLICATION NUMBER: US/10/110,731

CURRENT APPLICATION NUMBER: BP 99 120 484.3

PRIOR PALLAG DATE: 1999-10-15

NUMBER OF SEQ ID NOS: 3

SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO 2

LENGTH: 10
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ilarity 100.0%; Pred. No. 5.5e+06;
Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Synthetic Peptide US-10-447-161-117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09673795; Sequence 2, Application US/09673795; GENERAL INFORMATION: APPLICANT: TRIEBEL, FREDERIC
                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 9; Conservative
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ORGANISM: Homo sapiens
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Matches 9; Conserv
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US-09-673-795-1
IS-204-673-795-1
| Sequence 1. Application US/09673795
| GENERAL INFORMATION:
| APPLICANT: TRIEBEL, FREDERIC
| APPLICANT: TRIEBEL, FREDERIC
| TITLE OF INVENTION: MUTATED PEPTIDE COMPOUNDS, DERIVED FROM hsp70, USEFUL IN CANCER
| TITLE OF INVENTION: IMMUNOTHERAPY
| TITLE OF INVENTION: IMMUNOTHERAPY
| TITLE OF INVENTION: IMMUNOTHERAPY
| FILE REFERENCE: 03715.0069
| CURRENT APPLICATION NUMBER: PC/09/673,795
| PRIOR APPLICATION NUMBER: PC/FR99/00957
| PRIOR APPLICATION NUMBER: FR 98 05033
| PRIOR FILING DATE: 1998-04-22
| NUMBER OF SEQ ID NOS: 8
| SOFTWARE: Patentin Vers. 2.1
| SEQ ID NO 1
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TITLE OF INVENTION: THEN LYMPHOCYTES, A PROCESS FOR PREPARING THE SAME AND
TITLE OF INVENTION: THEN USE IN THERAPEUTICS
FILLE REFERENCE: WOB 99 EA IDM STRE
CURRENT APPLICATION NUMBER: US/10/110,731
CURRENT FILLING DATE: 12002-04-15
PRIOR PILLING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO 1
LENGTH: 9
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100.0%; Score 46; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+06;
Matches 9; Conservative 0; Mismatches 0; Indels
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APPLICANT: Wang, Rong-fu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/10110731 GENERAL INFORMATION:
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Matches 9; Conservative
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
CRGANISM: Homo sapiens
US-10-110-731-1
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CORGANISM: Homo sapiens
US-09-673-795-1
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US-10-447-161-117
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                          Matches
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Sequence 203858, Application US/10424599
GENERAL INFORMATION:
APPLICANT: La Rosa Thomas J
APPLICANT: Car Variation David K
APPLICANT: Car Variation David K
APPLICANT: Car Variation Vibua
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APPLICATION
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GRANEAL INFORMATION:
TITLE OF INVENTION: INFORMATION:
TITLE OF INVENTION: THEIR USE IN THERAPEUTICS
FILLS REFREENCE: WOR 99 BA IDM STRE
CURRENT APPLICATION NUMBER: US/10/110,731
PRIOR PILLOATION NUMBER: EP 99 120 484.3
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PARENTAL NOS: 3
SOFTWARE: PARENTAL NOS: 3
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LOCATION: (1)..(130)
OTHER INFORMATION: unsure at all Xaa locations
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Pred. No. 0.29
0; Mismatches
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                               SLFEGIDEY 9
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Matches 8; Conserv
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US-10-424-599-255293
                                                                                                                                                                              RESULT 9
US-10-110-731-3
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i Sequence 8, Application US/09673795

i GENERAL INFORMATION:

APPLICANT: TRIEBEL, FREDERIC

APPLICANT: GAUDIN, CATHERINE

TITLE OF INVENTION: IMMUNOTHERAPY

TITLE OF INVENTION: IMMUNOTHERAPY

FILE REFERENCE: 03715,0069

CURRENT APPLICATION NUMBER: US/09/673,795

CURRENT APPLICATION NUMBER: PCT/FR99/00957

FRIOR PILING DATE: 1999-04-22

PRIOR APPLICATION NUMBER: FR 98 05033

PRIOR APPLICATION NUMBER: R 98 05033

PRIOR PILING DATE: 1998-04-22

NUMBER OF SEQ ID NOS: 8

SOFTWARE: PATENTH VEYS: 2.1

SEQ ID NO 8

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APPLICANT: TRIBBEL, CATHERINE
TITLE OF INVENTION: MUTATED PROTIDE COMPOUNDS, DERIVED FROM hsp70, USEFUL IN CANCER TITLE OF INVENTION: INMUNOTHERAPY
TITLE OF INVENTION: INMUNOTHERAPY
FILE REPERBNCE: 03715.0069
CURRENT APPLICATION NUMBER: NS/09/673,795
CURRENT FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
RIOR FILING DATE: 1998-04-22
ROWNERS OF SEQ ID NOS: 8
SOFTWARE: PATCH IN VETS. 2.1
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                                                                                                                                                              100.0%; Score 46; DB 27; Length 10; 100.0%; Pred. No. 0.045; tive 0; Mismatches 0; Indels
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Pred. No. 5.5e+06;
0; Mismatches 1;
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Pred. No. 0.29;
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GENERAL INFORMATION:
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                                                                                                                                                                                                                                     9; Conservative
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TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
US-09-673-795-8
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; ORGANISM: Homo sapiens
US-09-673-795-7
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Matches 8; Conserva
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 8; Conserv
                                               ; ORGANISM: DS-10-110-731-2
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APPLICANT: Huang, Qian
APPLICANT: Huang, Qian
APPLICANT: Richmond, Joan F.L.
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APPLICANT: Richmond, Joan F.L.
APPLICANT: Richmond, Joan F.L.
APPLICANT: Palliser, Deborah
APPLICANT: Chen, Jianzhu
APPLICANT: Eisen, Herman N.
APPLICANT: Chen, Jianzhu N.
APPLICANT: Young, Richard A.
ITILE OF INVENTION: Protein Fusion Proteins Maps To A Discrete Domain and is TITLE OF INVENTION: Depote In Fusion Proteins Maps To A Discrete Domain and is TITLE OF INVENTION: CD4+T Cell-Independent
FILE REFERENCE: 0399.2006-003
CURRENT APPLICATION NUMBER: US/09/761,534A
CURRENT PILING DATE: 2001-01-16
PRIOR PILING DATE: 2000-10-14
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 4.0
SSG ID NO 12
LENGTH: 209
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Sequence 2553, Application US/60196712
GENERAL INFORMATION:
APPLICANT: Bonazzi, Vivien
APPLICANT: Bonazzi, Vivien
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILIR REPRESENCE: CLO004-13
FILIR REPRESENCE: CL0004-13
CURRENT APPLICATION NUMBER: 18/60/196,712
CURRENT FILING DATE: 2000-04-13
NUMBER OF SEQ ID NOS: 3846
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2253
INSTERN THE SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SECOND SE
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                                                                                          Length 208;
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                                                                                          DB 22;
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Pred. No. 9.7;
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US-09-761-534A-12
                                                                                          Score 42; DB 2
Pred. No. 9.5;
0; Mismatches
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88.9%;
                                                                                              91.3%;
; ORGANISM: Aplysia californica
US-09-791-537-3064
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Best Local Similarity 88.5
Matches 8; Conservative
                                                                                              Query Match 91.3
Best Local Similarity 88.5
Matches 8; Conservative
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Best Local Similarity
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ORGANISM: Unknown
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US-60-196-712-2253
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APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
APPLICANT: Debe, Derek
TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMBE
TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REPERENCE: 261/210
CURRENT APPLICATION NUMBER: US/09/791,537
CURRENT APPLICATION NUMBER: 2001-02-22
NUMBER OF SEQ ID NOS: 153055
SOFTWARE: Patentin version 3.0
SEQ ID NO 3064
LENGTH: 208
TYPE: PRT
                                   APPLICANT: Zhou Yihua APPLICANT: Zhou Yihua APPLICANT: Cao Yongwei TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement FILE REPERBNCE: 38-21(53223)B CURRENT APPLICATION NUMBER: US/10/424,599 CURRENT FILING DATE: 2003-04-28 NUMBER OF SEQ ID NOS: 285684 SEQ ID NOS: 285684 LENGTH: 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2.2471, Application US/09417507

Sequence 2.2471, Application US/09417507

GENERAL INFORMATION:
APPLICANT: KEITH G. WEINSTOCK ET AL.
TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ASPERGILLUS
TITLE OF INVENTION: FUNGATUS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: PATH99-10

CURRENT APPLICATION NUMBER: US/09/417,507

CURRENT PILING DATE: 1999-10-14

NUMBER OF SEQ ID NOS: 44312

SEQ ID NO 2.2471

LENGTH: 175
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Pred. No. 7.8;
0; Mismatches 1; Indels
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Pred. No. 7.7;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (1)..(174)
OTHER INFORMATION: unsure at all Xaa locations
PEATURE:
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88.9%;
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88.9%;
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
                      Kovalic David K
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CRGANISM: A.fumigatus
US-09-417-507-22471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 SLFEGIDIY 9
                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT ORGANISM: Glycine max
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US-09-417-507-22471
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                         APPLICANT:
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Search completed: September 15, 2004, 10:46:48 Job time: 282.368 secs

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2: /cgn2_6/ptodata/2/pubpaa/US07_NEW PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1335176 seqs, 320689617 residues
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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46
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 117, App Sequence 203858, Sequence 255293, Sequence 12, Appl Sequence 12, Appl Sequence 119, App Sequence 319, App Sequence 326, App Sequence 328, App Sequence 329, App Sequence 330, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 346, App Sequence 1256, App Sequence 1256, App
SUMMARIES	US-10-447-161-117 US-10-424-599-203858 US-10-445-599-255293 US-10-767-701-33352 US-09-761-5348-12 US-09-761-5348-12 US-10-328-953-31 US-10-328-953-319 US-10-328-953-329 US-10-328-953-329 US-10-328-953-329 US-10-328-953-329 US-10-328-953-329 US-10-328-953-329 US-10-328-953-329 US-10-328-953-329 US-10-328-953-329 US-10-328-953-329 US-10-328-953-329
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US-10-767-701-47005	US-10-132-556A-2	US-10-369-493-22298	m	4~25		US-09-935-642-1	US-09-919-039-146	2 US-10-380-408A-5	US-10-316-253-28	US-10-316-253-97	US-09-761-534A-10	US-10-369-493-1394	US-10-369-493-1760	US-10-451-467A-146	US-10-369-493-22772	US-10-425-114-62894	US-10-425-114-62493	US-10-425-114-62884	US-10-369-493-4146	US-10-437-963-193936	US-09-733-179A-11	US-09-919-039-204	US-10-755-889-396	US-10-437-963-193938	US-09-925-302-724	30	US-09-864-408A-242	US-10-264-049-4304	US-10-767-701-46700
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91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	91.3	89.1	89.1	89.1	89.1	89.1	89.1	89.1	84.8	84.8	84.8
42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	42	41	41	41	41	41	41	41	გ	39	39
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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US-10-47-161-117; Application US/10447161; Sequence 117, Application US/10447161; Sequence 117, Application No. US20040023314A1; Sequence 117, Application No. US20040023314A1; Sequence 117, Application No. US20040023314A1; Sequence Into Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Environmental Env
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| GENERAL INFORMATION:
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| APPLICANT: Huang, Qian |
| APPLICANT: Richmond, Joan F.L. |
| APPLICANT: Che, Bryan K. |
| APPLICANT: Che, Jianzhu |
| APPLICANT: Chen, Jianzhu |
| APPLICANT: Chen, Jianzhu |
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| APPLICANT: Chen, Jianzhu |
| APPLICANT: Poung, Richard A. |
| TITLE OF INVENTION: TO YOU CTL Elicitation By Heat Shock |
| TITLE OF INVENTION: CD4+T Cell-Independent |
| TITLE OF INVENTION: CD4+T Cell-Independent |
| TITLE OF INVENTION: CD4+T Cell-Independent |
| TITLE OF INVENTION: CD4+T Cell-Independent |
| TITLE OF INVENTION NUMBER: DC7/US00/32831 |
| PRIOR FILING DATE: 2000-12-01 |
| PRIOR FILING DATE: 2000-01-14 |
| NUMBER OF SEQ ID NOS: 25 |
| SOFTWARE: FastSEQ for Windows Version 4.0
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38-21(53535)B CURRENT APPLICATION NUMBER: US/10/767,701 CURRENT FILING DATE: 2004-01-29 NUMBER OF SEQ ID NOS: 63128 SEQ ID NO 33352 LENGTH: 181
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ITILE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
FILE REFERENCE: 11390/46101
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US-10-767-701-33352
                                                                                                                                                                                                                                                                                                                                                                    91.3%; Score 42; DB 16;
88.9%; Pred. No. 2.1;
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88.9%; Pred. No. 2.5;
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US-09-761-534A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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US-09-761-534A-12
'Sequence 12, Application US/09761534A
'Patent No. US20020146426A1
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Publication No. US20040071656A1
GENERAL INFORMATION:
APPLICANT: Wieland, Felix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                      Query Match 91.3
Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Sorghum bicolor
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Best Local Similarity
Matches 8; Conserv
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US-10-328-953-1
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APPLICANT: La Rosa Thomas J
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPRESENCE: 38-21(5323)
CURRENT APPLICATION NUMBER: US/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 255293
LENGTH: 174
                              APPLICANT: Zhou Yihua
APPLICANT: Zhou Yihua
APPLICANT: Cao Yongwei
TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFRENCE: 38 - 21 (53233) B
CURRENT APPLICATION NUMBER: U$/10/424,599
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 203858
LENGTH: 130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 42; DB 12; Length 130;
Pred. No. 1.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; CTHER INFORMATION: Clone ID: PAT_MRT3847_72551C.1.pep
US-10-424-599-255293
                                                                                                                                                                                                                                                                                                                                                                                                                                       , OTHER INFORMATION: Clone ID: PAT_MRT3847_26109C.1.pep
US-10-424-599-203858
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OTHER INFORMATION: unsure at all Xaa locations FEATURE:
                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: unsure
LOCATION: (1)..(130)
OTHER INFORMATION: unsure at all Xaa locations
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US-10-767-701-33352
; Sequence 33352, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
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88.9%;
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88.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 91.3
Best Local Similarity 88.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
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ORGANISM: Glycine max
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SLFEGIDIY 9
                                                                                                                                                                                                                                                                                      TYPE: PRT ORGANISM: Glycine max
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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; OTHER INFORMATION: fusion polypeptide: hsp70(1-381)-Gly-Ser-Gly-gp100(209-217:Met210
US-10-328-953-326
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APPLICANT: Wieland, Felix
APPLICANT: Wieland, Felix
APPLICANT: Wieland, Franz-Ulrich
TITLB OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
FILE REFERENCE: 11390/46101
CURRENT FILING DATE: 2002-12-23
CURRENT FILING DATE: 2001-12-28
PRIOR FILING DATE: 2001-12-28
PRIOR FILING DATE: 2001-12-28
PRIOR FLING DATE: 2001-12-28
PRIOR FLING DATE: 2002-04-12
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SOFTWARE: WordPerfect 8.0 for Windows
SEQ ID NO 326
LENTH: 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DATABASE ACCESSION NUMBER: Genbank GI:15277246; amino acids 1-381 of hsp70; DATABASE ENTRY DATE: 2001-08-22
US-10-328-953-319
                           TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 5.1;
0; Mismatches 1
                                         FILE REFERENCE: 11390/46101
CURRENT APPLICATION NUMBER: US/10/328,953
CURRENT APPLICATION NUMBER: US/10/328,953
CURRENT APPLICATION NUMBER: US 60/342,570
PRIOR APPLICATION NUMBER: US 60/342,570
PRIOR FILING DATE: 2001-12-28
PRIOR APPLICATION NUMBER: US 60/372,620
PRIOR FILING DATE: 2002-04-12
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-07-29
PRIOR FILING DATE: 2002-09-28
NUMBER OF SEQ ID NOS: 331
SOFTWARE: WORDPEFFECT 8.0 for Windows
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88.9%; Pred. No.
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Publication No. US20040071656A1
GENERAL INFORMATION:
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Best Local Similarity 88.9
Matches 8; Conservative
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Best Local Similarity 88.9
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 319
                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 381
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DATABASE ACCESSION NUMBER: GenBank GI:15277246; amino acids 5-381 of hsp70
DATABASE ENTRY DATE: 2001-08-22
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APPLICANT: Gibson, Bradford W.
APPLICANT: Gibson, Bradford W.
APPLICANT: Glann, Gaven W.
APPLICANT: Glann, Gaven W.
APPLICANT: Glann, Gaven W.
APPLICANT: Glann, Gaven W.
APPLICANT: Glann, Gaven W.
APPLICANT: Glann, Gaven W.
APPLICANT: Glann, Gaven W.
APPLICANT: Glann, Gaven W.
APPLICANT: Marnock, Dale E.
ITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION
ITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME
FILE REPREBUCE: 660088.465
CURRENT FILING DATE: 2003-04-04
NUMBER OF SEQ ID NOS: 3077
SOFTWARE FASLESQ for Windows Version 4.0
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Pred. No. 4.8;
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Pred. No. 4.9;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
CURRENT APPLICATION NUMBER: US/10/328,953
CURRENT FILING DATE: 2002-12-23
FRIOR APPLICATION NUMBER: US 60/342,570
FRIOR TILING DATE: 2001-12-26
FRIOR PLING DATE: 2001-12-28
FRIOR PLING DATE: 2001-12-28
FRIOR APPLICATION NUMBER: US 60/372,620
FRIOR APPLICATION NUMBER: US 60/372,620
FRIOR PLING DATE: 2002-04-12
FRIOR FILING DATE: 2002-04-12
FRIOR FILING DATE: 2002-09-29
FRIOR FILING DATE: 2002-09-28
NUMBER: OF SEQ ID NOS: 331
SEQ ID NO I
LENGTH: 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
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US-10-328-953-319
US-10-328-953-319
is Sequence 319, Application US/10328953
is Publication No. US20040071656A1
is GENERAL INFORMATION:
i APPLICANT: Wieland, Felix
i APPLICANT: Hartl, Franz-Ulrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.3%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Ghosh, Soumitra S.
APPLICANT: Fahy, Boin D.
APPLICANT: Zhang, Bing
APPLICANT: Gibson, Bradford W.
APPLICANT: Taylor, Steven W.
APPLICANT: Glann, Gary M.
APPLICANT: Warnock, Dale E.
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88.9%;
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Best Local Similarity 88.9
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Best Local Similarity 88.5
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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US-10-408-765A-763
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US-10-408-765A-763
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                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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Gaps

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sequence 329, Application US/10328953

publication No. US20040071656A1

GENERAL INFORMATION:

APPLICANT: Wieland, Felix

APPLICANT: Wieland, Felix

APPLICANT: Wieland, Felix

APPLICANT: Modulation of Heat-Shock-Protein-Based Immunotherapies

FILE REFERENCE: 11390/46101

CURRENT FILING DATE: 2002-12-23

PRIOR APPLICATION NUMBER: US 60/342,570

PRIOR PILING DATE: 2001-12-26

PRIOR PILING DATE: 2001-12-28

PRIOR FILING DATE: 2001-12-28

PRIOR FILING DATE: 2001-04-12

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-04-12

PRIOR FILING DATE: 2002-07-29

PRIOR FILING DATE: 2002-07-29

PRIOR FILING DATE: 2002-07-29

PRIOR PILING DATE: 2002-07-29
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APPLICANT: Wieland, Felix
APPLICANT: Wieland, Felix
TITLE OF INVENTION:
FILE REFERENCE: 11390/46101
CURRENT APPLICANTON WORDER: US/10/328,953
CURRENT APPLICANTON WHERE: US/10/328,953
CURRENT FILING DATE: 2002-12-23
FRIOR APPLICATION WHERE: US 60/342,570
PRIOR APPLICATION NUMBER: US 60/342,894
FRIOR PILING DATE: 2001-12-28
FRIOR PILING DATE: 2001-12-28
FRIOR PRILING DATE: 2002-04-12
FRIOR PLILING DATE: 2002-04-12
FRIOR APPLICATION NUMBER: US 60/372,620
FRIOR PLILING DATE: 2002-04-12
FRIOR PLILING DATE: 2002-04-12
FRIOR FILING DATE: 2002-04-29
FRIOR FILING DATE: 2002-04-29
FRIOR FILING DATE: 2002-03-39
FRIOR FILING DATE: 2002-07-29
FRIOR FILING DATE: 2002-07-29
FRIOR FILING DATE: 2002-07-39
FRIOR FILING DATE: 2002-07-39
FRIOR FILING DATE: 2002-07-39
FRIOR FILING DATE: 2002-07-39
FRIOR FILING DATE: 2002-07-39
FRIOR FILING DATE: 2002-07-39
FRIOR FILING DATE: 2002-09-38
FRIOR FILING DATE: 2002-09-38
FRIOR FILING DATE: 2002-09-38
FRIOR FILING DATE: 2002-09-38
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                                                                                   Gaps
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91.3%; Score 42; DB 12; Length 393; 88.9%; Pred. No. 5.1;
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                                                                                   Indels
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Publication No. US20040071656A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 88.9
Matches 8; Conservative
                Query Match
Best Local Similarity 88.9
Matches 8; Conservative
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                                                                                                                                                                          1 SLFEGIDIY 9
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US-10-328-953-330
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OTHER INFORMATION: fusion polypeptide: gp100(209-217:Met210)-Gly-Ser-Gly-hsp70(1-381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ## Squence 328, Application US/10328953

## Squence 328, Application US/10328953

## Squence 328, Application US/10328953

## Squence 328, Application No. US20040071656A1

## SPLICANT: Wieland, Felix

## APPLICANT: Wieland, Felix

## TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies

## TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies

## TITLE OF INVENTION: Worder: US/10/328,953

## CURRENT PILING DATE: 2002-12-23

## PRIOR PELICATION NUMBER: US 60/343,884

## PRIOR PELICATION NUMBER: US 60/343,884

## PRIOR PILING DATE: 2002-04-12

## PRIOR PILING DATE: 2002-04-12

## PRIOR APPLICATION NUMBER: US 60/399,342

## PRIOR PILING DATE: 2002-04-12

## PRIOR APPLICATION NUMBER: US 60/399,342

## PRIOR PILING DATE: 2002-09-28

## NUMBER OF SEQ ID NOS: 331

## NUMBER OF SEQ ID NOS: 331

## NUMBER OF SEQ ID NO 328

## DENGTH: 393

## NUMBER OF SEQ ID NO 328

## DENGTH: 393

## NUMBER OF SEQ ID NO 328

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## NUMBER OF SEQ ID NO 328

## NUMBER OF SEQ ID NO 328

## NUMBER OF SEQ ID NO 328
                                                                                                                                                                                                                                                             ## APPLICANT: Wieland, Felix

APPLICANT: Wieland, Felix

APPLICANT: Wieland, Felix

APPLICANT: Wieland, Felix

TITLE OF INVENTION: Modulation of Heat-Shock-Protein-Based Immunotherapies

FILE REFERENCE: 11390/46101

CURRENT APPLICATION NUMBER: US/10/328,953

CURRENT PILING DATE: 2002-12-23

FRIOR PELING DATE: 2001-12-26

PRIOR FILING DATE: 2001-12-26

PRIOR PILING DATE: 2001-12-28

PRIOR PILING DATE: 2001-12-28

PRIOR PILING DATE: 2001-0-28

PRIOR APPLICATION NUMBER: US 60/343,884

PRIOR PILING DATE: 2002-04-12

PRIOR PILING DATE: 2002-04-12

PRIOR PILING DATE: 2002-04-14

PRIOR FILING DATE: 2002-04-14

PRIOR FILING DATE: 2002-03-0-28

NUMBER OF SEQ ID NOS: 331

LENGTH: 393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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llarity 88.9%; Pred. No. 5.1;
Conservative 0; Mismatches 1; Indels
                                                                                                                                                 Sequence 327, Application US/10328953 Publication No. US20040071656A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  298 SLFEGIDFY 306
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Best Local Similarity
Matches 8; Conserv
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US-10-328-953-328
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Sequence 12366, Application US/10369493

Sequence 12366, Application US/10369493

Publication No. US20030233675A1

GENERAL INPORMATION:

APPLICANT: Gregory J.

APPLICANT: Glater, Steven C.

APPLICANT: Gregory J.

APPLICANT: Glater, Steven C.

APPLICANT: Gregory J.

APPLICANT: Glater, Steven C.

APPLICANT: Gregory J.

APPLICANT: Gregory J.

APPLICANT: Glater, Steven C.

APPLICANT: Gregory J.

APPL
                                                                                                                                           FEATURE:
COTHER INFORMATION: fusion polypeptide: hsp70(1-381)-Gly-Ser-Gly-COTHER INFORMATION: gp100(209-217:Met210)-Gly-Ser-Gly-tyrosinase(368-376:Asp370)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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US-10-108-260A-3466
; Sequence 3466, Application US/10108260A
; Publication No. US20040005560A1
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
; TITLE OF INVENTION: No. US20040005560A1e1 full length cDNA
; FILE REFERENCE: H1-A01.06
; CURRENT APPLICATION NUMBER: US/10/108,260A
; UNRENT FILING DATE: 2002-03-27
; NUMBER OF SEQ ID NOS: 5458
; SOFTWARE: PATCHIL Ver. 2.1
; SEQ ID NO 3466
; LENGTH: 476
                                                                                                                                                                                                                                                                                                                                           Query Match 91.3%; Score 42; DB 12; Length 405; Best Local Similarity 88.9%; Pred. No. 5.2; Matches 8; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91.3%; Score 42; DB 15; Length 476; 88.9%; Pred. No. 6.3; 1. Indels
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91.3%; Score 42; DB 15; Length 516;
Best Local Similarity 88.9%; Pred. No. 6.9;
Matches 8; Conservative 0; Mismatches 1; Indels
                                                                   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: PRT
; ORGANISM: Aspergillus nidulans
US-10-369-493-12366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 88.9%;
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286 SLFEGIDFY 294
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ORGANISM: Homo sapiens
US-10-108-260A-3466
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SEQ ID NO 330
                                           LENGTH:
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284 SLFEGIDFY 292
 1 SLFEGIDIY 9
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Search completed: September 15, 2004, 10:51:17 Job time: 82 secs

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GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
               Copyright
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OM protein - protein search, using sw model

September 15, 2004, 10:32:27; Search time 14.2105 Seconds (without alignments) 32.696 Million cell updates/sec Run on:

US-09-673-795-1 46 1 SLFEGIDIY 9 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

389414 segs, 51625971 residues Searched:

389414 Total number of hits satisfying chosen parameters:

DB seq length: 0 DB seq length: 2000000000 Minimum Maximum I

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

lssued_Patents AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

scription	CTT acretmen	Secretary 2	Seguence 37	Sequence 14,		Sequence 533.	Seducinos	Sequence 9,
	9-107-532A-	US-08-797-358B-3	US-08-441-139-14	US-09-513-783A-174	US-09-134-000C-5332	US-09-107-5328-6410	US-09-343-494-9	118-09-358-3837-11
DB	4	m	Н	4	4	4	4	٠ 4
Query Match Length DB	226	643	646	890	321	319	1284	1284
	89.1	89.1	84.8	84.8	78.3	76.1	71.7	71.7
Score	41	41	39	39	36	35	33	33
Result No.	гł	7	m	4	S	9	7	80

tion	125. 127.	٥
Description	Sequence Seq	acidence
SUMMARIES	US-09-107-552A-7155 US-08-797-58B-3 US-08-741-139-14 US-08-741-139-14 US-09-134-000C-5332 US-09-107-552A-6410 US-09-134-000C-5332 US-09-343-494-9 US-09-343-494-9 US-09-343-494-9 US-09-343-494-9 US-08-19-573-2 US-08-19-573-2 US-08-19-573-2 US-08-780-89-5 US-08-780-89-5 US-08-443-883A-22 US-08-443-883A-22 US-08-443-883A-22 US-08-455-011B-22 US-08-455-011B-22 US-09-465-901-26 US-09-465-901-26 US-09-465-901-26 US-09-465-901-26 US-09-465-901-26 US-09-465-901-26 US-09-465-901-26 US-09-465-901-26 US-09-134-001C-5538 US-09-138-32A-51-14	110
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US-09-107-532A-7125

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US-09-543-681A-5019	US-08-727-338C-38	US-08-936-165A-294	US-09-328-352-5812	US-08-438-753B-24	US-08-443-883A-24	US-08-631-328-24	US-08-455-524B-24	US-08-455-021B-24	US-09-045-467-24	US-09-205-264-2	US-09-604-073-2	US-09-489-847-155	US-09-543-681A-8261	US-09-198-452A-605	US-09-328-352-4229	
4 4	[†] "	4	4	7	٦	C)	Ŋ	N	m	m	4	4	4	4	4	4
579	789	98	90	95	95	95	95	95	95	161	191	225	254	261	279	290
67.4	67.4	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2	65.2
31	31	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30
2 2	30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

APPLICANT: Lynn A Doucette-Stamm and David Bush TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS THERAPEUTICS CORPORATION CURRENT APPLICATION DATA:
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30-Jun-1998
PRIOR APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
ATTORNEY/AGENT INFORMATION:
NAME: AATHIGLIO, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION: NAME/KEY: misc feature LOCATION: (B) LŌCATION 1...226 SRQUENCE DESCRIPTION: SEQ ID NO: 7125: ORGANISM: Enterococcus faecium COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
COMPATING SYSTEM: COMPUTER: PC Sequence 7125, Application US/09107532A Patent No. 6583275 GENERAL INFORMATION: NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSEE: GENOME THERAPRUT:
STREET: 100 Beaver Street
CITY: Waltham
STATE: Massachusetts
COUNTRY: USA LENGTH: 226 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: YES ORIGINAL SOURCE: US-09-107-532A-7125 FEATURE RESULT 1

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REFERENCE/DOCKET NUMBER: 8646
REFERENCE/DOCKET NUMBER: 8646
TELEPHONE: 516-742-4343
TELERAX: 516-742-4366
TELEX: 230 901 SANS UR
INPORMATION POR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 77.8
Matches 7; Conservative
                                                                  CITY: Garden City
STATE: NY
COUNTRY: USA
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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286 SLYEGIDFY 294
CORRESPONDENCE ADDRESS:
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                      ADDRESSEE: SCULLY,
STREET: 400 Garden
CITY: Garden City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-441-139-14
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                                                                                 Gaps
                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08797358B
Sequence 3, Application US/08797358B
Patent No. 6268478
GENERAL INFORMATION:
APPLICANT: Adams, John
TITLE OF INVENTION: INTRACELLULAR VITAMIN D BINDING PROTEIN NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Campbell & Flores Lip
STREET: 4770 La Johla Village Drive, Suite 700
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/797,358B
FILING DATE: 11-Feb-1997
CLASSIFICATION NUMBER: US 60/011,491
FILING DATE: 12-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REGISTRATION NUMBER: 31,815
TELECOMUNICATION INFORMATION:
TELECOMUNICATION INFORMATION:
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Pred. No. 3.8;
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Sequence 14, Application US/08441139
Sequence 14, Application US/08441139
GENERAL INFORMATION:
APPLICANT: Wittrup, Dr. Karl D.
APPLICANT: Robinson, Anne S.
TITLE OF INVENTION: METHODS FOR INCREASING SECRETION OF TITLE OF INVENTION: RECOMBINANTLY EXPRESSED PROTEINS
NUMBER OF SEQUENCES: 20
                             Score 41; DB 4; Length 226;
Pred. No. 1.2;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: unknown;
MOLECULA TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-08-797-358B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 643 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: California
COUNTRY: United States
ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS
                                     89.1%;
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Best Local Similarity 77.8'
                 Query Match
Best Local Similarity 87.5-
"Lag 7; Conservative
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                                                                                                                                                                          189 LFEGIDAY 196
                                                                                                                                2 LFEGIDIY 9
                                                                                                                                                                                                                                                       RESULT 2
US-08-797-358B-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
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Gaps
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US-09-513-783A-174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       84.8%; Score 39; DB 1; Length 646; 77.8%; Pred. No. 9.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
US-09-513-783A-174
US-09-513-783A-174
Sequence 174, Application US/09513783A
Patent No. 641659
GENERAL INFORMATION:
APPLICANT: Gapuliano, Kenneth A.
TITLE OF INVENTION: A System for Cell Based Screening
TITLE OF INVENTION: A System for Cell Based Screening
TITLE OF INVENTION: B System for Cell Based Screening
TURENT APPLICATION NUMBER: US/09/513,783A
CURRENT FILING DATE: 2000-02-25
NUMBER OF SEQ ID NOS: 180
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                          WEDTUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Rolease FILING DATE: 15-MAY-1995
RIGHT APPLICATION DATE: 08-041,139
RIGHT APPLICATION NUMBER: US 08/089,997
FILING DATE: 06-UUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: DIGHGLIO, Frank S.
REGISTRATION NUMBER: 31,346
E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
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NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1...319
SEQUENCE DESCRIPTION: SEQ ID NO: 6410:
US-09-107-532A-6410
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APPLICANT: Jegla, Timothy J.
APPLICANT: Jegla, Timothy J.
APPLICANT: Jeckenden, Alan
ITILE OF INVENTION: Human Elk, a Voltage-Gaté
TITLE OF INVENTION: Human Elk, a Voltage-Gaté
FILE REFERENCE: 018512-001330US
CURRENT APPLICATION NUMBER: US 60/91,469
EARLIER FILING DATE: 1999-06-30
EARLIER FILING DATE: 1999-07-01
EARLIER FILING DATE: 1999-01-21
NUMBER OF SEQ ID NOS: 9
SEQ ID NO 9
SEQ ID NO 9
LENGTH: 1284
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
                                                                                                                                                                                                                                                                                                                                                                       US-09-343-494-9; Sequence 9, Application US/09343494; Patent No. 6413741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Drosophila melanogaster
                                                                                                                                                                    h 76.1%;
Similarity 75.0%;
6; Conservative 2
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126 LFQGIDIF 133
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Best Local Similarity
Matches 7; Conserv
                                         FEATURE:
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US-09-107-532A-6410
US-09-107-532A-6410
Sequence 6410, Application US/09107532A
Fatent No. 6583275
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
                   Sequence 5332, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO TITLE OF INVENTION: EXTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS TITLE OF INVENTION NUMBER: US/09/134,000C
FILE REPERENCE: 0379-08-13
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR APPLICATION NUMBER: US 60/055,778
RICH RELING DATE: 1997-08-15
SOFTWARE: PatentIn version 3.1
SEQ ID NOS: 6812
SEQ ID NOS: 5332
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Pred. No. 18;
4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:
ADDRESSES: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
CITY: Waltham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/09/107,532A
FILING DATE: 30-Jun-1998
FILING DATE: 14 May 1998
FILING DATE: 14 May 1998
FILING DATE: 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneke
REGISTATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: 40,489
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM IYPE: CD/ROM ISO9660
COMPUTER: PC
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 319 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 6410: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                               78.3%;
55.6%;
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Best Local Similarity 55.0.
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28 SIFDGIEVY 36
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      US-09-134-000C-5332
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Sequence 11, Application US/09358383C
| Sequence 11, Application US/09358383C
| Patent No. 6518398
| GENERAL INFORMATION:
| APPLICANT: Curtis, Rory A.J.
| TITLE OF INVENTION: NOVEL POTASSIUM CHANNEL MOLECULES AND USES THEREFOR
| TITLE OF INVENTION: NUMBER: US/09/358,383C
| CURRENT APPLICATION NUMBER: US/N 09/119,855
| PRIOR APPLICATION NUMBER: US/N 09/119,855
| NUMBER OF SEQ ID NOS: 36
| SOFTWARE: PatentIn Ver. 2.0
| LENGTH: 1284
                                                                                                                                                                                                                                                                                                                                                                                                                                           a Voltage-Gated Potassium Channel Subunit
                                                          Gaps
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Score 35; DB 4; Length 319;
Pred. No. 28;
2; Mismatches 0; Indels
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US-09-358-383C-11
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Query Match 69.6%;
Best Local Similarity 71.4%;
Matches 5; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
US-08-919-573-4
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                                                    COUNTRY: USP
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           Score 33; DB 4; Length 1284; Pred. No. 3.2e+02; 0; Mismatches 2; Indels
                                                                                                                    US-08-919-573-2

US-08-919-573-2

Sequence 2, Application US/08919573

Fatent No. 6346392

GENERAL INFORMATION:

APPLICANT: Burnham, Martin, Karl Russel

TITLE OF INVENTION: NOVEL GLUTAMINE TRANSPORT

TITLE OF INVENTION: ATP-BINDING PROTEIN

NUMBER OF SEQUENCES: 6

CORRESPONDENCES: 6

CORRESPONDENCES: 6

CORRESPONDENCE ADDRESS:

STREET: 997 Lenox Drive, Building 3, Suite 210

CITY: Lawrenceville

CITY: Lawrenceville

COUNTRY: USA

ZIP- NOTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/08919573
Patent No. 6346392
GENERAL INFORMATION:
APPLICANT: Burnham, Martin, Karl Russel
TITLE OF INVENTION:
TITLE OF INVENTION: ATP-BINDING PROTEIN
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version 2.0
CURTERNY EPPLICATION DATA:
APPLICATION NUMBER: US/08/919,573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REFERENCE/DOCKET NUMBER: F50597
TELEPHONE: 609-520-3214
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS: LENGTH: 244 amino acids TYPE: amino acid STRANDEDNESS: single
                71.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
Query Match
Best Local Similarity 77...
7; Conservative
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                                                                                        1 SLFEGIDIY 9
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63 IFEGVDI 69
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Matches 5; Conserv
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APPLICANT: KUSTERS-VAN SOMBREN, MARGO A.
APPLICANT: KUSTER, YVONNE
APPLICANT: KESTER, HERMANUS C.M.
APPLICANT: VISSER, JACOB
APPLICANT: VISSER, JACOB
APPLICANT: VISSER, JACOB
APPLICANT: VISSER, JACOB
APPLICANT: VISSER, JACOB
APPLICANT: VINDING AND EXPRESSION OF THE
TITLE OF INVENTION: CLONING AND EXPERSION OF THE
TITLE OF INVENTION: CLONING AND EXPERSION OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ..
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STREET: 2000 Pennsylvania Avenue N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/290,976A
FILING DATE: 17-OCT-1994
CLASSIFICATION: 435
ADDRESSER: Dechert Price & Rhoads
STREET: 997 Lenox Drive, Building 3, Suite 210
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
ODFRATING SYSTEM: DOS
ODFRARE: Fast-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,573
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bloom, Allen
REGISTRATION NUMBER: 29,135
REGISTRATION NUMBER: P50597
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
TELEPHONE: 609-520-3214
TELERAX:
TELERAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/08290978A Patent No. 5624834 GENERAL INFORMATION:
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0
                                                                                                                                                                                                                                                                                                                                                                    Length 452;
                                                                                                                                                                                                                                                                                                                                                             69.6%; Score 32; DB 1; Length 452
85.7%; Pred. No. 1.6e+02;
ive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUUNTER: DC
COUNTER: DC
COUNTER: DC
COMPUTER READABLE FORM:
MEDIUW TYPE: CIPOPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,869
FILING DATE: 24-JAN-1997
CLASSIFICATION NUMBER: US 08/290,978
FILING DATE: 17-OCT-1994
ATTORNEY/AGENT INPORMATION:
NAME: MURASHIGE, KATE H:
REGISTRATION NUMBER: 24.50
FEGISTRATION NUMBER: 4615-0044.00
TELLEPHONE: (202) 887-1500
TELLEPHONE: (202) 887-1500
TELLEPHONE: (202) 887-1500
TELLEPHONE: (202) 887-1503
TELLEPHONE: GOOD NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VAN OOYEN, ALBERT J.J.
APPLICANT: ROLIN, CLAUS
TITLE OF INVENTION: CLONING AND EXPRESSIO
TITLE OF INVENTION: EXO-POLYGALACTURONASE
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FORESTER
STREET: 2000 Pennsylvania Avenue N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KUSTERS-VAN SOMEREN, MARGO A.
MULLER, YVONNE
KESTER, HERMANUS C.M.
VISSER, JACOB
                                                                             4615-0044.00
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 4615-
FELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEPHONE: (202) 887-1500
TELERX: 90-4030
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
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Patent No. 5830737
GENERAL INFORMATION:
APPLICANT: KUSTERS-VAN SOMEREN,
                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 85.7
Matches 6; Conservative
                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
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; MOLECULE TYPE: protein
US-08-780-869-5
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203 LFDGIDI 209
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APPLICANT:
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US-08-780-869-5
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Patent No. 6380370
Patent No. 6380370
Patent No. 6380370
Patent No. 6380370
Patent No. 6380370
Patent No. 6380370
Patent No. 6380370

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1999-08-13
PRIOR PAPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR PELICH DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5482
LENGTH: 722
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TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
CURRENT APPLICATION NUMBER: US/09/457,046B
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.1
                                                                 Gaps
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                         Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69.6%; Score 32; DB 3; Length 458; 66.7%; Pred. No. 1.6e+02; Live 1; Mismatches 2; Indels
                   Score 32; DB 2; Length 452
Pred. No. 1.6e+02;
1; Mismatches 0; Indels
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85.7%; Pred. No. 2.7e+02;
Live 1; Mismatches 0
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ORGANISM: Staphylococcus epidermidis
                                                                                                                                                                                                                             ; Sequence 61, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
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US-08-438-753B-22
Sequence 22, Application US/08438753B
Patent No. 5705363
GENERAL INFORMATION:
                     69.6%;
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Query Match
Best Local Similarity 85.,
'.e 6; Conservative
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Best Local Similarity 66.7
Matches 6; Conservative
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203 LFDGIDI 209
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Matches 6; Conserv
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US-09-134-001C-5482
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LENGTH: 458
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INDIVIDUAL ISOLATE: predicted amino acid coding sequence; INDIVIDUAL ISOLATE: of SEQ ID NO:21 (HulfNtau6).
US-08-438-753B-22
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67.4%; Score 31; DB 1; Length 99;

Best Local Similarity 66.7%; Pred. No. 48;

Matches 6; Conservative 1; Mismatches 2; Indels
APPLICANT: Imakawa, Kazuhito
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Interferon Tau Compositions and
TITLE OF INVENTION: Methods of Use
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STREE: CA
COUNTRY: UGA
CITY: PALO ALTO
STREE: ADDRESS:
MEDIUM TYPE: FLORDY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: FLORDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IDM PC compatible
CLEASIFICATION NUMBER: US 08/139,891
FILING DATE: 10-MAX-1995
CLIASIFICATION NUMBER: US 07/3847,741
FILING DATE: 10-MAX-1995
FILING DATE: 09-MAR-1992
FILING DATE: 09-MAR-1992
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FILING DATE: 01-MAR-1993
FILING DATE: 01-MAR-199
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Search completed: September 15, 2004, 10:36:49
Job time : 15.2105 secs 83 SYFQGIHIY 91

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Gaps .

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5.1.6
Compugen Ltd.
GenCore version (c) 1993 - 2004
                                                   OM protein - protein search, using sw model
            Copyright
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Run on:

September 15, 2004, 10:29:20; Search time 47.8421 Seconds (without alignments) 53.153 Million cell updates/sec

US-09-673-795-1 46 Title:

1 SLFEGIDIY 9 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

seq length: 0 seq length: 200000000 Minimum DB Maximum DB

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2003as:* geneseqp2003bs:* geneseqp2004s:* A_Geneseq_29Jan04:* geneseqp1990s:* geneseqp2000s:* geneseqp2001s:* geneseqp1980s:* geneseqp2002s:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4 AAE12986	6 ABU8971	6 ARPANAGE	COLUMN O	b ABK4039	6 ABR40399	6 ABR4040(7 ADD46498	7 ADE57092	7 ADD45046	7 ADD47457	000000000000000000000000000000000000000	ADD4/455	8 ADE76981	3 AAB23650	5 ABG93094	6 ARRSO671	in the contract of	6 ABK52/61	2 AAR03928	6 ARR40401	A PART C	/ ABM/3664	6 ABR40402
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91.3	91.3	91.3		0.10	91.3	91.3	91.3	91.3	91.3	91.3	91		91.3	91.3	91.3	91.3	01.0		91.3	91,3	6		91.3
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26	27	28	oc	1 0	30	31	32	33	34	35	36	1 0	7 5	χ Υ	39	40	4.1	1 (42	43	44		4. C

ALIGNMENTS

Heat shock protein 70 amino acid residues 286-294. AAY44199 standard; peptide; 9 AA. 15-FEB-2000 (first entry) AAY44199; RESULT 1 AAY44199

Human; heat shock protein 70; hsp70; identification; tumour; mutation; I cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen.

Homo sapiens

WO9954464-A1.

28-OCT-1999.

99WO-FR000957. 22-APR-1999; 98FR-00005033. 22-APR-1998;

(INSR) INST ROUSSY GUSTAVE.

Gaudin C; Triebel F,

WPI; 2000-013251/01.

Identifying mutant peptides from heat-shock protein 70, for treatment of cancer.

Claim 10; Page 6; 56pp; French.

This peptide corresponds to amino acid residues 286-294 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce a tumour-specific T-cell response, comprises: (i) amplifying hsp70 encoding DNA from one or more tumours; (ii) cloning the amplified sequences into a vector that can be replicated in bacteria; (iii) sequencing fragments in each cultured bacterial colony to identify any hsp70 mutations, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer,

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The amino acid sequence of fragment 1 relating to position 286-294 of
thuman heat shock protein 70 (HSEP70) is given. The new invention relates
thuman heat shock protein 70 (HSEP70) is given. The new invention relates
to lymphocytes which recognise cells of a patient in which overexpression
of HSP has been induced. Overexpression of HSP leads to a substantial
increase in the numbers of HSPs and HSP pitopes presented on the
pericellular membrane. Recognition of increased numbers of HSP epitopes
or cell pericellular membranes by lymphocytes elicits a cytotoxic
response which kills the target cells. As a further embodiment of the
invention, HSP70 epitopes are mutated prior to being loaded into antigen
or presenting cells. This has the effect of increasing the immune response
to HSP and helps direct the immune response to specific cells, (e.g.
cancer cells). HSP70 fragments are useful for treating cancer or
intracellular infections by vaccination. The tolerance of the organism to
the tumour or to the virus associated HSP is broken using an immunogenic
mutated form of HSP and induction of a stress on the target tumoural or
intracellular infected cells
                                                                                                                                                                                                                                                                                        0;
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particularly solid cancers (carcinoma, sarcoma, melanoma, neuroblastoma, cancers of head and neck, particularly kidney cancer). The peptides may also be used to increase the proportion of tumour-specific cytotoxic T lymphocytes in a cell culture and/or induce these calls to secrete cytotoxic factors (specifically interleukin-2, interferon-gamma and tumour necrosis factor), particularly where the cells are used to stimulate immune defences. The method identifies peptides with high immunogenicity and high specificity for particular HLA (human leucocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSP, HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 1.
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                                                                                                                                                                                                                                                    Length 9;
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                                                                                                                                                                                                                                                  100.0%; Score 46; DB 3; L
100.0%; Pred. No. 1.4e+06;
cive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB97601 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-SEP-2000; 2000WO-EP009530.
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                                                                                                                                                                                                                                                                                               9; Conservative
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The invention relates to a composition (I) comprising an immune effector cell and a cell penetrating peptide (CPP) associated with an antigen or antibody. Also included are (1) a vaccine comprising (I), CPP associated with an antigen, and a pharmaceutically acceptable carrier and (2) preparing a composition for a disease, by providing (I) and CPP associated with an antigen for disease, and introducing the antigens are, for example, tumour antigen enters into the cell. The antigens are, for example, tumour antigen enters into the cell. The antigens are, is a second to the antigen of the composition is useful for enhancing immunity in an animal to a disease, by administering a mature dendritic cell comprising CPP associated with an antigen to disease, to the animal comprising the administration, animal is protected from disease, where the animal comprises both CD4+ and CD8+ I cells. It is also useful for treating a lime.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disease (e.g. cancer, tumour, melanoma, thymoma, lymphoma, sarcoma, lung cancer, non-Hodgkin's lymphoma, leukaemia, Hodgkin's lymphoma, uterine cancer, cervical cancer, bladder cancer, kidney cancer, adenocarcinoma, breast cancer, prostate cancer, ovarian cancer and pancreatic cancer). The animal is further subjected to a cancer treatment including surgery, radiation, chemotherapy or gene therapy. The administration of (1), preferably dendritic cell is prior to, subsequent to or concurrent with,
                                                                                                                                                                                                                                                                                                                                                                                                                 Cell penetrating peptide; cancer; tumour; melanoma; thymoma; antigen; lymphoma; laukaemia; Hodgkin's lymphoma; leukaemia; Hodgkin's lymphoma; uterine cancer; cervical cancer; bladder cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel composition for treating a disease in an animal, comprises an immune effector cell and cell penetrating peptide associated with an antigen or antibody.
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kidney cancer; adenocarcinoma; breast cancer; prostate cancer; ovarian cancer; pancreatic cancer; epitope; vaccine; dendritic cell; tumour infiltrating lymphocyte; TIL; human leukocyte antigen; HLA;
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                                                                                                                                                                                                                                                                                                                                                                               Human HSP70-2m class I HLA tumour-restricted antigen peptide.
                                            100.0%; Score 46; DB 4; Length 9; 100.0%; Pred. No. 1.4e+06;
                                                                                   Indels
                                                                                     ;
0
                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure, Page 20; 61pp; English.
                                                                                                                                                                                                                                                                   ABG79108 standard; peptide; 9 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-FEB-2002; 2002WO-US005212.
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                                                                                         Conservative
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                              Query Match
Best Local Similarity
Best Local 9; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; human.
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              Sequence 9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                15-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-AUG-2002
                                                                                                                                                                                                                                                                                                             ABG79108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang R;
                                                                                                                                                                                                                                  RESULT 3
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0;
                                                                                                                                                                                      Human; heat shock protein 70; hsp70; identification; tumour; mutation; T cell response; amplification; vector; bacterium; cancer; allele; cytotoxic factor; interleukin; interferon; tumour necrosis factor; HLA; immune defence; immunogenicity; specificity; human leucocyte antigen.
the cancer treatment. The present sequence is a tumour antigen derived epitope for inclusion in the composition of the invention
                                                          Gaps
                                                          ;
0
                                          Length 9;
                                                        Indels
                                       ; Score 46; DB 5; Le
; Pred. No. 1.4e+06;
0; Mismatches 0;
                                                                                                                                                                       Heat shock protein 70 amino acid residues 286-295.
                                                                                                                          AAY44200 standard; peptide; 10 AA.
                                        100.0%;
                                                                                                                                                                                                                                                                             99WO-FR000957,
                                                                                                                                                        (first entry)
                                                      9; Conservative
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                                                                     1 SLFEGIDIY 9
                                                                                   SLFEGIDIY
                                              Best Local Similarity
                       Sequence 9 AA;
                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                             WO9954464-A1
                                                                                                                                                                                                                                                                           22-APR-1999;
                                                                                                                                                         15-FEB-2000
                                                                                                                                                                                                                                                            28-OCT-1999,
                                                                                                                                         AAY44200;
                                      Query Match
                                                      Matches
                                                                                                          8X333
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This peptide corresponds to amino acid residues 286-295 of the human heat shock protein 70 (hsp70). The invention relates to a method of identifying peptides, derived from hsp70 that stimulate a tumour-specific T cell response. Identification of the hsp70 peptides that have at least one mutation or alteration compared with the native sequence, and induce the tumour-specific T-cell response, comprises: (i) amplifying hsp70 concluding DNA from one or more tumours; (ii) cloning the amplified encoding DNA from one or more tumours; (ii) cloning the amplified sequences into a vector that can be replicated in bacteria; (iii) esquencing fragments in each cultured bacterial colony to identify any comparions, and (iv) determining the immunogenicity of the mutant peptides identified. The peptides, optionally formulated with an agent that induces cellular stress, are used for treatment of cancer, cancers of head and neck, particularly kidney cancer). The peptides may cancers of head and neck, particularly kidney cancer). The peptides may lymphocytes in a cell culture and/or induce these cells to secrete tumour necrosis factors (specifically interleukin-2, interfacton-gamma and cytomour expecification) particularly where the cells are used to immunogenicity and high specificity for particular HIA (human leucocyte Identifying mutant peptides from heat-shock protein 70, for treatment of Claim 10; Page 6; 56pp; French. cancer.

Sequence 10 AA;

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The amino acid sequence of fragment 2 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates to 1ymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP pitopes presented on the pericellular membranes. Recognition of increased numbers of HSP epitopes on cell pericellular membranes by lymphocytes elicits a cytotoxic invention, HSPN epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSPV fragments are useful for treating cancer or intracellular infections by vaccinated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or
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                                                                                                                                                                                                                                                                                                                  HSP; HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 2.
                                                        Gaps
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0
                       DB 3; Length 10;
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                                                    0; Indels
                                                                                                                                                                                                                                                                                     Heat shock protein 70 (HSP70) peptidic fragment 2.
                   100.0%; Score 46; DB 3;
100.0%; Pred. No. 0.0086;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.
                                                                                                                                                                                          AAB97602 standard; peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 15; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-2000; 2000WO-EP009530.
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                                                   Conservative
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Query Match
Best Local Similarity
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                                                                                SLFEGIDIY
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Best Local Similarity
Matches 9; Consery
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                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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98FR-00005033.

22-APR-1998;

(INSR) INST ROUSSY GUSTAVE.

Triebel F, Gaudin C; WPI; 2000-013251/01.

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Human hsp70 peptide p20 (residues 286-305).
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                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABM73781;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    The amino acid sequence of fragment 3 relating to position 286-295 of human heat shock protein 70 (HSP70) is given. The new invention relates human heat shock protein 70 (HSP70) is given. The new invention relates to lymphocytes which recognise cells of a patient in which overexpression of HSP has been induced. Overexpression of HSP leads to a substantial increase in the numbers of HSPs and HSP epitopes presented on the concellular membranes by lymphocytes elicits a cytotoxic response which kills the target cells. As a further embodiment of the invention, HSP70 epitopes are mutated prior to being loaded into antigen presenting cells. This has the effect of increasing the immune response to HSP and helps direct the immune response to specific cells, (e.g. cancer cells). HSP70 fragments are useful for treating cancer or intracellular infections by vaccination. The tolerance of the organism to the tumour or to the virus associated HSP is broken using an immunogenic mutated form of HSP and induction of a stress on the target tumoural or intracellular infected cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                  bymphocytes useful for treating cancer, recognizes specifically transformed human cells with induced and increased membrane expression of
                                                                                                                                       HSP, HSP70; heat shock protein 70; cancer; chronic infectious disease; vaccine; HSP-peptide complex; tumour; peptidic fragment; lymphocyte; cytotoxic response; epitope; antigen presenting cell; fragment 3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91.3%; Score 42; DB 4; Length 10;
88.9%; Pred. No. 0.058;
iive 0; Mismatches 1; Indels
                                                                                                                 Heat shock protein 70 (HSP70) peptidic fragment 3.
                                                                                                                                                                                                                                                                                                               (IDMI-) IDM IMMUNO-DESIGNED MOLECULES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABR82812 standard; peptide; 20 AA.
                                                AAB97603 standard; peptide; 10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 15; 21pp; English.
                                                                                                                                                                                                                                                                29-SEP-2000; 2000WO-EP009530.
                                                                                                                                                                                                                                                                                          99EP-00120484
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                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SLFEGIDIY 9
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                               heat shock protein.
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                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABR82812
                                                                      AAB97603;
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ABR82812
                         RESULT 6
                                    AAB97603
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human heat-shock protein 70 (hsp70). The hsp70 peptide fragments of human heat-shock protein 70 (hsp70). The hsp70 peptides provide reliable differentiation between diabetes types I and II. The peptides induce a shift of the T cell response from Th1 (proinflammatory) to Th2 (antiinflammatory). They can be used (a) for treatment or prevention of autoimmune diseases, especially type I diabetes but also systemic lupus erythematorsus, multiple sclerosis and rheumatoid arthritis; and (b) for diagnosing presence or onset of these diseases. Isolated T cells may be activated in vitro with (A), or with heat-shock protein 70 and the responding cells are selected, attenuated and then returned to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sarley; single nucleotide polymorphism; SNP; genotype-phenotype analysis.
Heat-shock protein 70; hsp70; antidiabetic; human; immunosuppressive; dermatological; antiinflammatory; neuroprotective; antirheumatic; antiarthritic; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New peptides from human heat-shock protein 70, useful for treatment, prevention and diagnosis of autoimmune disease, specifically type I diabetes.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 42; DB 7; Length 20; Pred. No. 0.12;
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(YEDA ) YEDA RES & DEV CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cohen IR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 33; 49pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-DEC-2002; 2002WO-IB005403.
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                                                                                                                                                                                                                                                                                                                                     24-FEB-2003; 2003WO-IL000143.
                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-2002; 2002IL-00148401.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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Matches 8; Conservative
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The present invention relates to oligonucleotide clones originating in barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype analysis, isolation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published-pct-sequences
                                                                                                                                                                                                                          Single nucleotide polymorphism sites in barley varieties and DNA sequences containing them for analysis and identification of barley varieties and production of barley transformants with desired
                                                                                                                                                                                                                                                                                                                          Disclosure, SEQ ID XX, 284pp, Japanese.
20-DEC-2001; 2001JP-00387131.
20-DEC-2001; 2001JP-00403299.
20-DEC-2001; 2001JP-00403300.
27-SEP-2002; 2002JP-0037515.
                                                                                                                                               Kohara Y;
                                                                                                  (UYNI-) UNIV JAPAN OKAYAMA.
                                                                                                                                                                                   WPI; 2003-587127/55
                                                                                                                                             Takeda K,
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                                Gaps
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0
            Score 42; DB 7; Length 438;
Pred. No. 3.6;
0; Mismatches 1; Indels
                               1; Indels
           91.3%;
88.9%;
Query Match
Best Local Similarity 88.20,
Local 8, Conservative
                                                               SLFEGIDFY 300
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                                             SLFEGIDIY
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ABM73972 standard; protein; 454 AA. (first entry) 17-0CT-2003 ABM73972;

RESULT 9 ABM73972

Barley; single nucleotide polymorphism; SNP; genotype-phenotype analysis. DNA clone originating in barley containing SNP sequence #382.

Hordeum vulgare

WO2003057877-A1

17-JUL-2003

16-DEC-2002; 2002WO-IB005403

2001JP-00387059 20-DEC-2001;

20-DEC-2001; 2001JP-00387111. 20-DEC-2001; 2001JP-00403299. 20-DEC-2001; 2001JP-00403300. 27-SEP-2002; 2002JP-00327515.

(UYNI-) UNIV JAPAN OKAYAMA. Takeda K, Sato K,

WPI; 2003-587127/55

DNA barley Single nucleotide polymorphism sites in barley varieties and I sequences containing them for analysis and identification of I varieties and production of barley transformants with desired characteristics.

Disclosure, SEQ ID XX; 284pp; Japanese.

The present invention relates to oligonucleotide clones originating in barley (Hordeum vulgare) which contain single nucleotide polymorphisms (SNP). The oligonucleotides may be used for analysis of SNPs among barley varieties, identification of particular varieties and genotype-phenotype ransformation of specific genes and creation of new varieties by transformation of barley varieties with them and production of new barley varieties with desired properties. The present sequence represents an oligonucleotide clone sequence featured in the specification. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published-pct-sequences

Sequence 454 AA;

Gaps ö 7; Length 454; 1; Indels DB 7 Mismatches Score 42; Pred. No. 0; 91.3%; 8; Conservative Local Similarity Query Match Matches

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à 원

AAY88410 standard; protein; 554 AA. (first entry) 31-JUL-2000 AAY88410; RESULT 10

Human heat shock protein SHSP70 amino acid sequence.

Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; chromosome 14922-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70. Human;

Homo sapiens

JP2000069999-A.

07-MAR-2000

99JP-00257146 01-JUN-1995;

(HOKE-) HOKEN KAGAKU KENKYUSHO KK.

95JP-00158581

01-JUN-1995;

2000-264458/23

N-PSDB; AAA15622

Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application,

Disclosure; Fig 3; 11pp; Japanese.

This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 1462-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome

Sequence 554

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Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
                                                                                                                                                                                                                                                                                                         This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome
chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42; DB 3; Length 554;
Pred. No. 4.7;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                       Example; Fig 2; 11pp; Japanese.
                                                                                                                                                                              (HOKE-) HOKEN KAGAKU KENKYUSHO
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88.9%;
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Best Local Similarity 88.5
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 554 AA;
                                                                                                                                                                                                                        N-PSDB; AAA15621
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                                                                        JP2000069999-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-JUN-1995;
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                                               Homo sapiens.
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                                                                                                                                                      01-JUN-1995;
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                                                                                                   07-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome
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                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress;
                                                                                                                                                                                                                                                                             Human; heat shock protein; HSP70; chromosome 6p21.3-22; stress; chromosome 14q22-24; transcription; rheumatism; schizophrenia; depression; nephrotic syndrome; SHSP70.
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                         Length 554;
                                                  1; Indels
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                         DB 3;
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Pred. No. 4.7;
0; Mismatches
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                                                                                                                                                                          AAY88413 standard; protein; 554 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 6; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                   99JP-00257146.
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                          91.3%;
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les 8; Conserv
                                                                              1 SLFEGIDIY
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Best Local Similarity
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Gaps

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Abnormal transcription of intracellular HSP70mRNA under acute and chronic continuous load of stress in a human being and its application.
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                                                                                                                                                                                                                                          Human heat shock protein SHSP70 amino acid sequence.
AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOKE-) HOKEN KAGAKU KENKYUSHO KK.
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the proliferation of cells. Modulation of the activity of the JNK phosphatase or Hsp72 is used to treat a proliferative disorder such as cancers (e.g., leukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 activity can also be administered to treat premalignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp72 function are administered to a patient having a disease or disorder mediated by an increase of Hsp72 expression or activity relative to normal levels. The present sequence represents human Hsp72 used in the exemplifications of the invention

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Gaps

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Length 624; Indels

Score 42; DB 3; Pred. No. 5.3;); Mismatches

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Conservative

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Matches

Sest Local Similarity

Query Match

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Sequence 624 AA;

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286 SLFEGIDFY 294

91.3%; 88.9%;

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This sequence represents the human heat shock protein SHSP70 amino acid sequence. Human heat shock proteins are located on chromosomes 6p21.3-22 and 14q22-24. The invention relates to the abnormal transcription of intracellular HSP70mRNA under acute and chronic stress load in a human. The abnormal transcription of HSP70 can be used in the improvement of stress and response and diagnosis of stress diseases including rheumatisms, schizophrenia, depression and nephrotic syndrome
                                                                                                                                                                                                                                                                                                                                                               Human Hsp72; heat shock protein 72; chromosome 6p21.3; Hsp72 inhibitor; expression modulator; JNK phosphatase inhibitor; antiproliferative; drug screening; cancer; leukaemia; lymphoma; solid tumour; sarcoma; carcinoma; breast cancer; prostate cancer; premalignant condition.
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                                                                                                                                         Score 42; DB 3; Length 554;
Pred. No. 4.7;
                                                                                                                                                                  1; Indels
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                          (heat shock protein 72).
                                                                                                                                                                                                                                                                   AAB23252 standard; protein; 624 AA.
Disclosure; Fig 5; 11pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0125046P.
                                                                                                                                          91.3%;
88.9%;
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                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                 8; Conservative
                                                                                                                                                                                                           200 SLPEGIDEY 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Volloch VZ, Sherman M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PHYL-) PHYLOGENY INC.
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                                                                                                                                       Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                      1 SLFEGIDIY
                                                                                                                 Sequence 554 AA;
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                                                                                                                                                                                                                                                                                                                                          Human Hsp72
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                                                                                                                                                                                                                                                                                                                   29-JAN-2001
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AAB23252
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8 x C C C C C C C C X X S
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AAR03930 standard; protein; 634 AA.

RESULT 15

AAR03930

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According to the legend of Fig 2, the G. gallus HSP sequence has 635 amino acid residues, the sequence itself has only 634, including "O" (?) at position 634. Fig. 2 provides an alignment of heat shock proteins from a variety of organisms: I. M. hyopneumoniae (Mnyhsp70 - AAR03922); 2. Bacillus megaterium (Bmehsp70 - AAR03923); 3. B. coli (dnaK - AAR03924); 4. T. cruzi (tc70kd - AAR03925); 5. T. cruzi (AAR03926); 6. Rat rattus (rathsp70 - AAR03925); 9. Gallus gallus (chkhsp70 - AAR03930); 10. Zea mays (mzehsp70 - AAR03931); 11. Serratia marcescens (smahsp70 - AAR03931); 11. Serratia marcescens (smahsp70 - AAR03932); vecines and diagnosis involving e.g. Trypanosoma, Mycoplasma and
                                                                                                                                                                                                                                                                                                                                                                                                                        Proteins homologous to heat shock proteins of Trypanosoma cruzi - used in vaccines and diagnosis for species of e.g. muco-plasma or mycobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure, Fig 2.1-2.14; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                     Sias S;
                                                                                                                                                                                                                                                                                                                                                                   Dragon E, Faulds D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacteria species
                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1990-115820/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 634 AA;
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The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell which overexpresses Hsp72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of Hsp72.

Optionally, Hsp72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72-mediated JNK phosphatase activation, comprising contacting a test compound with a cell which determining if the compound inhibits JNK phosphatase activity. The invention additionally encompasses compositions compressing an inhibitor of Hsp72 or JNK phosphatase activity. The compounds identified as inhibitors of Hsp72 or JNK phosphatase activity are useful for inhibiting

/note= "residue given as "O" in specification"

88US-00243474. 88US-00243474

12-SEP-1988; 12-SEP-1988; (CODO-) CODON

벙

Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hsp72 useful for treating cancers such as leukemia, lymphoma.

WPI; 2000-647056/62.

N-PSDB; AAA97541

Example, Fig 16B, 77pp, English.

Location/Qualifiers

Misc-difference

WO9002564-A. 22-MAR-1990

gallus

Gallus

Hsp70; heat shock protein; Trypanosoma cruzi; vaccines; HSP.

Gallus gallus HSP (chkhsp70).

30-AUG-1990 (first entry)

AAR03930;

0; Gaps Query Match 91.3%; Score 42; DB 2; Length 634; Best Local Similarity 88.9%; Pred. No. 5.4; Matches 8; Conservative 0; Mismatches 1; Indels

0;

δ Dp Search completed: September 15, 2004, 10:34:08 Job time: 50.3421 secs